

NOVEL ALCOHOL/ALDEHYDE DEHYDROGENASES

5

FIELD OF THE INVENTION

The present invention relates to recombinant enzymes, particularly, novel recombinant alcohol/aldehyde dehydrogenases (hereinafter referred to as AADH or AADHs) having alcohol and aldehyde dehydrogenase activity. The present invention also relates to novel recombinant DNA molecules encoding AADHs, recombinant expression
10 vectors containing said DNAs, and recombinant organisms containing said recombinant DNA molecules and/or said recombinant expression vectors. Furthermore, the present invention relates to a process for producing recombinant AADHs and a process for producing aldehydes, carboxylic acids and ketones, especially, 2-keto-L-gulonic acid (herein after referred to as 2KGA) by utilizing said recombinant enzymes, and a process for
15 producing aldehydes, carboxylic acids and ketones, especially, 2KGA by utilizing said recombinant organisms.

BACKGROUND OF THE INVENTION

2-KGA is an important intermediate for the production of L-ascorbic acid (vitamin
20 C). For example, 2KGA can be converted into ascorbic acid according to the well-known Reichstein method. Numerous microorganisms are known to produce 2KGA from D-sorbitol or L-sorbose. Japanese Patent Publication No. 51-40154 (1976) discloses the production of 2KGA from D-sorbitol by microorganisms of the genus *Acetobacter*, *Bacterium* or *Pseudomonas*. According to Acta Microbiologica Sinica 21(2), 185 - 191
25 (1981), 2KGA can be produced from L-sorbose by a mixed culture of microorganisms, especially, *Pseudomonas striata* and *Gluconobacter oxydans*. European Patent Publication

No. 0221 707 discloses the production of 2KGA from L-sorbose by *Pseudogluconobacter saccharoketogenes* with and without concomitant bacteria. European Patent Publication No. 0278 447 discloses a process for the production of 2KGA from L-sorbose by a mixed culture, which is composed of strain DSM No. 4025 (*Gluconobacter oxydans*) and DSM
5 No. 4026 (a *Bacillus megaterium* strain). European Patent Publication No. 88116156 discloses a process for the production of 2KGA from L-sorbose by *Gluconobacter oxydans* DSM No. 4025.

From *G. oxydans* DSM No. 4025, AADH was purified and characterized to
10 catalyze the oxidation of alcohols and aldehydes, and was thus capable of producing the corresponding aldehydes and ketones from alcohols, and carboxylic acids from aldehydes (see European Patent Publication No. 606621). More particularly, the AADH catalyzed the oxidation of L-sorbose to 2KGA via L-sorbosone. The physico-chemical properties of the purified sample of the AADH were as follows:

- 15 a) Optimum pH: about 7.0 - 9.0
- b) Optimum temperature: about 20°C - 40°C
- c) Molecular weight : 135,000 +/- 5,000 dalton
(Consisting of two subunits in any combination of such α -subunit
and β -subunit, each having a molecular weight of 64,500 +/- 2,000
20 and 62,500 +/- 2,000, respectively)
- d) Substrate specificity: active on primary and secondary alcohols and aldehydes including L-sorbose, L-sorbosone, D-sorbitol, D-glucose, D-mannitol, D-fructose, DL-glyceraldehyde, ethanol, 1-propanol, 1-butanol, 1-pentanol, 1-hexanol, 1-heptanol, 2-propanol, 2-butanol,
25 propionaldehyde, PEG1000, PEG2000, PEG4000, PEG6000 and polyvinyl alcohol

e) Prosthetic group: pyrroloquinoline quinone

f) Isoelectric point: about 4.4

Once the genes coding for said AADH have been cloned, they can be used for the
5 construction of a recombinant organism capable of producing a large amount of the
recombinant AADH or the various aldehydes, ketones and carboxylic acids, especially,
2KGA. However, there have been no reports so far of the cloning of such genes.

SUMMARY OF THE INVENTION

10 The present invention relates to novel recombinant AADHs having alcohol and
aldehyde dehydrogenase activity. Comprised by the present invention are novel
recombinant molecules encoding the AADHs; recombinant expression vectors containing
said DNAs; recombinant organisms carrying the DNAs and/or recombinant expression
vectors; a process for producing the recombinant AADHs; and a process for producing
15 aldehydes, carboxylic acids and ketones, especially, 2KGA utilizing the recombinant
AADHs or the recombinant organisms.

More particularly, an aspect of the present invention concerns a recombinant
enzyme having alcohol and aldehyde dehydrogenase activity which comprises one or more
20 recombinant polypeptides which contain an amino acid sequence selected from SEQ ID NO
5, SEQ ID NO 6, SEQ ID NO 7, SEQ ID NO 8 and functional derivatives thereof which
contain addition, insertion, deletion and/or substitution of one or more amino acid residues,
wherein the recombinant polypeptides have said alcohol and aldehyde dehydrogenase
activity.

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The present invention also provides AADH enzymes which comprise chimeric recombinant polypeptides that are a chimeric combination of at least two of the following amino acid sequences identified by SEQ ID NO 5, SEQ ID NO 6, SEQ ID NO 7, SEQ ID NO 8, and functional derivatives thereof which contain addition, insertion, deletion and/or substitution of one or more amino acid residues, wherein the recombinant polypeptides have said alcohol and aldehyde dehydrogenase activity.

Another aspect of the present invention concerns a recombinant DNA molecule encoding at least one recombinant polypeptide containing an amino acid sequence selected from SEQ ID NO 5, SEQ ID NO 6, SEQ ID NO 7, SEQ ID NO 8, chimeric combinations of at least two of the following amino acid sequences identified by SEQ ID NO 5, SEQ ID NO 6, SEQ ID NO 7, SEQ ID NO 8, and functional derivatives thereof which contain addition, insertion, deletion and/or substitution of one or more amino acid residues, wherein said recombinant polypeptides have said alcohol and aldehyde dehydrogenase activity.

The recombinant DNA molecules of the present invention contain DNA sequences encoding the polypeptides with alcohol and aldehyde dehydrogenase activity as disclosed, e.g., in the sequence listings herein as well as their complementary strands, or those which include these sequences, DNA sequences which hybridize under standard conditions with such sequences or fragments thereof, and DNA sequences which because of the degeneracy of the genetic code, do not hybridize under standard conditions with such sequences but which code for polypeptides having exactly the same amino acid sequence.

Further aspects of the present invention concern a recombinant expression vector which carries one or more of the recombinant DNA molecules defined above and a recombinant organism which carries the recombinant expression vector defined above and/or carries one or more recombinant DNA molecules on a chromosome.

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A further aspect of the present invention concerns a process for producing a recombinant enzyme having an alcohol and aldehyde dehydrogenase activity as defined above, which comprises cultivating a recombinant organism defined above in an appropriate culture medium and recovering said recombinant enzyme.

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Another aspect of the present invention concerns a process for producing an aldehyde, ketone or carboxylic acid product from a corresponding substrate which comprises converting said substrate into the product by the use of a recombinant organism as defined above.

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Moreover another aspect of the present invention concerns a process for producing 2-keto-L-gulonic acid which comprises the fermentation of a recombinant organism as defined above in an appropriate medium containing L-sorbose and/or D-sorbitol.

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Another aspect of the present invention concerns a process for producing an aldehyde, ketone or carboxylic acid product from a corresponding substrate which comprises the incubation of a reaction mixture containing a recombinant enzyme of the present invention.

Furthermore another aspect of the present invention concerns a process for producing 2-keto-L-gulonic acid which comprises the incubation of a reaction mixture containing a recombinant AADH and L-sorbose and/or D-sorbitol.

5 It is also an object of the present invention to provide an intermediate, i.e., 2-keto-L-gulonic acid, for the production of vitamin C whereby a process for the production of 2-keto-L-gulonic acid as described above is effected and the 2-keto-L-gulonic acid obtained by such process is transformed into vitamin C (L-ascorbic acid) by methods known in the art.

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Before describing the present invention in more detail a short explanation of the attached figures is given.

BRIEF DESCRIPTION OF THE DRAWINGS

15 Figure 1 schematically illustrates the structures of the recombinant expression vectors each carrying a recombinant DNA molecule which encodes a recombinant Enzyme A or B of the present invention.

Figure 2 schematically illustrates the structures of recombinant expression vectors each carrying a recombinant DNA molecule which encodes a chimeric enzyme of the
20 present invention.

Figure 3 schematically illustrates the structures of the material plasmids each carrying a recombinant DNA molecule containing tandem structural genes of Enzyme A and Enzyme B for constructing the chimeras by a homologous recombination method.

Figure 4 illustrates the recombinant expression vectors each encoding the chimera
25 Enzyme sA2, Enzyme sA21, Enzyme sA22, or Enzyme sB, using preferable codon usage, wherein these chimeric enzymes have structures denoted by the following particular amino

acid residue numbers of the mature amino acid sequences of Enzyme A and Enzyme B:
Enzyme sA2 has the structure of Enzyme A amino acid residue Nos. 1-135, Enzyme B
amino acid residue Nos. 136 - 180 and Enzyme A amino acid residue Nos. 180 - 556;
Enzyme sA21 has the structure of Enzyme A amino acid residue Nos. 1-128, Enzyme B
5 amino acid residue Nos. 129 - 180 and Enzyme A amino acid residue Nos. 180 - 556;
Enzyme sA22 has the structure of Enzyme A amino acid residue Nos. 1-125, Enzyme B
amino acid residue Nos. 126 - 180 and Enzyme A amino acid residue Nos. 180 - 556; and
Enzyme sB has the structure of Enzyme A amino acid residue Nos. 1 - 95, Enzyme B
amino acid residue Nos. 96 - 180 and Enzyme A amino acid residue Nos. 180 - 556.

10 Figure 5 shows the alignment of the amino acid sequences of the mature Enzyme A
and Enzyme B.

Figure 6 illustrates the construction schemes of the recombinant genes encoding
chimeric enzymes of the present invention.

Figure 7 shows the restriction map of the genes of Enzymes A and B.

15 Figure 8 illustrates the construction of chimeric genes by homologous
recombination of two AADH genes in vivo at the conserved nucleotide sequences in both
genes.

Figure 9 shows a site-directed mutagenesis to introduce a *Bam*HI site upstream of
the Enzyme B gene.

20 Figure 10 illustrates a scheme of the replacement of the promoter for the Enzyme B
gene.

Figure 11 shows graphs illustrating the substrate specificity of chimeric enzymes of
the invention.

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DETAILED DESCRIPTION OF THE INVENTION

The AADH genes of the present invention encode AADH enzymes capable of catalyzing the oxidation of various alcohols and aldehydes as described above.

- 5 Specifically, particular genes encoding AADHs present in *Gluconobacter* were cloned and expressed. Alternative organisms from which AADH genes can be obtained, may be identified by one skilled in the art using the teachings of the present invention.

A specific and preferred *Gluconobacter oxydans* strain has been deposited at the
10 Deutsche Sammlung von Mikroorganismen in Göttingen (Germany) under DSM No. 4025.

Moreover, a subculture of the strain has also been deposited in the Agency of Industrial Science and Technology, Fermentation Research Institute, Japan, under the
15 deposit No.: FERM BP-3812. European Patent publication No. 0278 477 discloses the characteristics of this strain.

The AADH genes and the recombinant microorganisms utilized in the present invention can be obtained by the following steps:

- 20 (1) Cloning the AADH genes from a chromosomal DNA by colony- or plaque-hybridization, PCR cloning, Western-blot analysis, Southern-blot hybridization and the like;
- (2) Determining the nucleotide sequences of such AADH genes by usual methods and
25 constructing recombinant expression vectors which contain and express AADH genes efficiently; and

(3) Constructing recombinant microorganisms carrying recombinant AADH genes on recombinant expression vectors or on chromosomes by transformation, transduction, transconjugation and electroporation.

5 The materials and the techniques applicable to the above aspect of the present invention are exemplified in details as described in the following:

A total chromosomal DNA can be purified by a procedure well known in the art (Marmur J., J. Mol. Biol. 3:208, 1961). Then, a genomic library of the strain for such
10 genes can be constructed with the chromosomal DNA and the vectors described below in detail. The genes encoding AADHs can be cloned in either plasmid or phage vectors from the total chromosomal DNA by the following methods:

(i) determining the partial amino acid sequences of the purified enzyme, according to the
15 sequence information, synthesizing the oligonucleotides, and selecting the objective gene from the gene library by Southern-blot-, colony-, or plaque-hybridization;

(ii) by amplifying the partial sequence of the desired gene by polymerase chain reaction (PCR) with the oligonucleotides synthesized as described above as the primers and with the
20 PCR product as a probe, selecting the complete sequence of the objective gene from the gene library by Southern-blot-, colony-, or plaque-hybridization;

(iii) by preparing the antibody reacting against the desired enzyme protein by such a method as previously described, e.g. in Methods in Enzymology, vol. 73, p 46, 1981, and
25 selecting the clone which expresses the desired polypeptide by immunological analysis including Western-blot analysis; and

(iv) by aligning the amino acid sequences of the homologs to the one of the desired enzyme, selecting the amino acid sequences which are well conserved, synthesizing the oligonucleotides encoding the conserved sequences, amplifying the partial sequence of the desired gene by PCR with the above oligonucleotides as the primers, and selecting the complete sequence as described above (ii).

The nucleotide sequence of the desired gene can be determined by a well known method such as the dideoxy chain termination method with the M13 phage (Sanger F., et al., Proc. Natl. Acad. Sci. USA, 74:5463-5467, 1977).

By using the information of the so determined nucleotide sequence (in consideration of the codon usage) a gene encoding evolutionally divergent alcohol/aldehyde dehydrogenases, can be isolated from a different organism by colony- or Southern-hybridization with a probe synthesized according to the amino acid sequence deduced from said nucleotide sequence or by the polymerase chain reaction with primers also synthesized according to said information, if necessary.

To express the desired gene or generally speaking the desired DNA sequence of the present invention efficiently, various promoters can be used; for example, the original promoter of said gene, promoters of antibiotic resistance genes such as the kanamycin resistant gene of Tn5 (Berg, D. E., and C. M. Berg. 1983. Bio/Technology 1:417-435), the ampicillin resistant gene of pBR322, a promoter of the beta-galactosidase gene of *Escherichia coli* (lac), trp-, tac- trc-promoter, promoters of lambda phages and any promoters which can be functional in the hosts consisting of microorganisms including bacteria such as *E. coli*, *P. putida*, *Acetobacter xylinum*, *A. pasteurianus*, *A. aceti*, *A. Hansenii* and *G. oxydans*, mammalian and plant cells.

Furthermore other regulatory elements, such as a Shine-Dalgarno (SD) sequence (for example, AGGAGG etc. including natural and synthetic sequences operable in the host cell) and a transcriptional terminator (inverted repeat structure including any natural and synthetic sequence operable in the host cell) which are operable in the host cell into which
5 the coding sequence will be introduced can be used with the above described promoters.

DNA encoding a signal peptide containing from about 15 to about 50 amino acid residues can be used to obtain expression of periplasmic AADH polypeptides. DNA encoding a signal peptide can be selected from any natural or synthetic sequence operable in
10 the host cell.

A wide variety of host/cloning vector combinations may be employed in cloning the double-stranded DNA. Suitable cloning vectors are generally plasmids or phage which contain a replication origin, regulatory elements, a cloning site including a multi-cloning
15 site and selection markers such as antibiotic resistance genes including resistance genes for ampicillin, tetracycline, kanamycin, streptomycin, gentamicin, spectinomycin, etc.

Preferred vectors for the expression of the DNA sequences of the present invention in *E. coli* are selected from any vectors usually used in *E. coli*, such as pBR322 or its
20 derivatives including pUC18 and pBluescript II, pACYC177 and pACYC184 (J. Bacteriol., 134:1141-1156, 1978) and their derivatives, and a vector derived from a broad host range plasmid such as RK2 and RSF1010. A preferred vector for the expression of the DNA sequences of the present invention in *Gluconobacter* including *G. oxydans* DSM No. 4025 and *P. putida* is selected from any vectors which can replicate in *Gluconobacter*
25 and/or *P. putida*, as well as a preferred cloning organism such as *E. coli*. The preferred vector is a broad-host-range vector such as a cosmid vector like pVK102 and its derivatives

and RSF1010 and its derivatives, and a vector containing a replication origin functional in *Gluconobacter* and another origin functional in *E. coli*. Copy number and stability of the vector should be carefully considered for stable and efficient expression of the cloned gene and also for efficient cultivation of the host cell carrying the cloned gene. DNA molecules
5 containing transposable elements such as Tn5 can be also used as a vector to introduce the DNA sequence of the present invention into the preferred host, especially on a chromosome. DNA molecules containing any DNAs isolated from the preferred host together with the desired DNA sequence of the present invention are also useful to introduce the desired DNA sequence of the present invention into the preferred host,
10 especially on a chromosome. Such DNA molecules can be transferred to the preferred host by transformation, transduction, transconjugation or electroporation.

Useful hosts may include microorganisms, mammalian cells, plant cells and the like. Preferable microorganisms, are bacteria such as *E. coli*, *P. putida*, *A. xylinum*, *A.*
15 *pasteurianus*, *A. aceti*, *A. hansenii*, *G. oxydans*, and any Gram-negative bacteria which are capable of producing recombinant AADHs. In accordance with the present invention, functional equivalents, subcultures, mutants and variants of said microorganism can also be used. Preferred strains are *E. coli* K12 and its derivatives, *P. putida* or *G. oxydans* DSM No. 4025.

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The functional AADH encoding DNA sequence of the present invention is ligated into a suitable vector containing a regulatory region such as a promoter and a ribosomal binding site operable in the host cell described above using well-known methods in the art to produce an expression plasmid. Structures of such recombinant expression vectors are
25 specifically shown in Figs. 1, 2, 4, and 10.

To construct a recombinant microorganism carrying a recombinant expression vector, various gene transfer methods including transformation, transduction, conjugal mating (Chapters 14 and 15, Methods for general and molecular bacteriology, Philipp Gerhardt et al. ed., American Society for Microbiology, (1994), and electroporation can be used. The method for constructing a recombinant organism may be selected from the methods well-known in the field of molecular biology. Usual transformation systems can be used for *E. coli*, *Pseudomonas* and *Acetobacter*. A transduction system can also be used for *E. coli*. Conjugal mating systems can be widely used in Gram-positive and Gram-negative bacteria including *E. coli*, *P. putida* and *G. oxydans*. A preferred conjugal mating method is described in WO89/06688. The conjugation can occur in liquid media or on a solid surface. The preferred recipient is selected from *E. coli*, *P. putida* and *G. oxydans* which can produce active AADHs with a suitable recombinant expression vector. The preferred recipient for 2KGA production is *G. oxydans* DSM No. 4025. To the recipient for conjugal mating, a selective marker is usually added; for example, resistance against nalidixic acid or rifampicin is usually selected.

The AADHs provided by the present invention catalyze the oxidation of alcohols and aldehydes, and are thus capable of producing aldehydes, ketones or carboxylic acids from corresponding substrates. More particularly, the AADHs provided by the present invention can catalyze the oxidation of L-sorbose to 2KGA via L-sorbose and/or the oxidation of D-sorbitol to L-sorbose.

The present invention provides AADHs that include one or more of the following enzymes: Enzyme A, Enzyme A', Enzyme A'', and Enzyme B, which contain the amino acid sequences shown in SEQ ID NO 5, SEQ ID NO 6, SEQ ID NO 7, and SEQ ID NO 8, respectively, and functional derivatives thereof that have alcohol and aldehyde

dehydrogenase activity, i.e., for example can oxidize substrates to aldehydes, carboxylic acids and/or ketones. Furthermore, the AADHs herein include chimeric recombinant polypeptides having any number of and/or combination of amino acid sequences identified by SEQ ID NOS. 5, 6, 7, 8 and functional derivatives thereof that have alcohol and
5 aldehyde dehydrogenase activity, i.e., for example can oxidize substrates to aldehydes, carboxylic acids and/or ketones.

Chimeric recombinant polypeptides encoding the AADHs of the present invention can be produced by any conventional methods known in the art. For example, the
10 chimeras can be prepared by combining two or more parts of DNA sequences of the present invention in vitro at the conserved restriction site in both sequences with restriction enzymes and T4-ligase as shown in Fig. 6, or by recombining two AADH genes in vivo at the conserved nucleotide sequences in both genes as shown in Fig. 8.

15 Functional derivatives of SEQ ID NOS. 5, 6, 7 and 8 contain addition, insertion, deletion and/or substitution of one or more amino acid residues of those sequences. Such functional derivatives can be made by conventional methods known in the art such as chemical peptide synthesis or by recombinant means; for example, those methods disclosed by Sambrook et al. (Molecular Cloning, Cold Spring Harbour Laboratory Press, New
20 York, USA, second edition 1989). Amino acid exchanges in proteins and peptides which do not generally alter the activity of such molecules are known in the state of the art and are described, for example, by H. Neurath and R.L. Hill in "The Proteins" (Academic Press, New York, 1979, see especially Figure 6, page 14). The most commonly occurring exchanges are: Ala/Ser, Val/Ile, Asp/Glu, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val,
25 Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, Asp/Gly as well as these exchanges in reverse.

The functional derivatives of the AADH polypeptides also include polypeptides with additional polypeptides at the N-terminal, C-terminal and/or inside region of the AADH polypeptides. Enzyme B, Enzyme A/B25, and Enzyme A/B3 fused with cytochrome *c* polypeptides (17 - 18 kDa) of *G. oxydans* DSM 4025 at the C-terminus
5 showed comparable AADH activities with their corresponding enzymes lacking the cytochrome *c* polypeptides i.e., Enzyme B described in Example 4 in the conversion of D-sorbitol to L-sorbose, and Enzyme A/B25 and Enzyme A/B3 both described in Example 14 in the conversion of L-sorbose to 2KGA. Thus, a relatively long polypeptide can be added or inserted to the AADHs provided by the present invention to form enzymes having
10 comparable AADH activity.


The functional derivatives of the AADH polypeptides described above can have preferred characteristics such as a desired substrate specificity, higher affinity to a substrate, lower affinity to an inhibitory compound, higher stability against temperature
15 and/or pH, and higher catalytic speed. As described in the working examples below, such derivatives would improve the productivity of the desired products. The alcohol and aldehyde dehydrogenase activity of enzymes that include recombinant polypeptides which contain amino acid sequences that are functional derivatives of SEQ ID NOS. 5, 6, 7, and/or 8 can be determined by conventional methods known in the art, such as the
20 preferred standard assay described herein.

The enzymatic recombinant polypeptides of the present invention are usually produced in the form of dimers. Such dimers include homodimers of Enzyme A, A', A" or B, or the derivatives including chimeras, and heterodimers consisting of two different
25 recombinant polypeptides mentioned above. Thus the recombinant enzymes of the present invention also contain one or more of said homodimers and/or heterodimers.

The recombinant DNA molecules encoding the AADH polypeptides of the present invention contain DNA sequences selected from SEQ ID NO 1, SEQ ID NO 2, SEQ ID NO 3 and SEQ ID NO 4, as well as their complementary strands, or those which include these sequences, DNA sequences which hybridize under standard conditions with such
5 sequences or fragments thereof and DNA sequences, which because of the degeneracy of the genetic code, do not hybridize under standard conditions with such sequences but which code for polypeptides having exactly the same amino acid sequence.

"Standard conditions" for hybridization mean in this context the conditions which are
10 generally used by one skilled in the art to detect specific hybridization signals and which are described, e.g. by Sambrook et al., "Molecular Cloning" second edition, Cold Spring Harbor Laboratory Press 1989, New York. Such "standard conditions" are preferably stringent hybridization and non-stringent washing conditions, or more preferably, stringent hybridization and stringent washing conditions familiar to those skilled in the art and which
15 are described, e.g. in Sambrook et al. (s.a.).

The DNA sequences encoding the AADHs of the present invention can be made by conventional methods known in the art, such as, for example, the polymerase chain reaction by using primers designed on the basis of the DNA sequences disclosed herein. It
20 is understood that the DNA sequences of the present invention can also be made synthetically as described, e.g. in EP 747 483.



In accordance with the present invention, the DNA molecules encoding the AADH polypeptides described herein can be gene-homologs resulting from degeneracy of the genetic code or any sequence of natural, synthetic or recombinant origin which has significant homology to the AADH genes. The DNA sequence derivatives can be

5 functional mutants of the polypeptides identified by SEQ ID NO 5, SEQ ID NO 6, SEQ ID NO 7 and SEQ ID NO 8 which contain addition, insertion, deletion and/or substitution of one or more amino acid residues, wherein the enzymatic polypeptides have alcohol and aldehyde dehydrogenase activity. The mutant genes can be prepared by any conventional method, such as, for example, treating AADH genes with a mutagen such as ultraviolet

10 irradiation, X-ray irradiation, γ -ray irradiation or contact with a nitrous acid, N-methyl-N'-nitro-N-nitrosoguanidine (NTG), or other suitable mutagens, or isolating a clone occurring by spontaneous mutation or by standard methods of in vitro mutagenesis known in the art.

Enzyme A, A', A", and B genes, which have the nucleotide sequences shown in

15 SEQ ID NOS. 1, 2, 3, and 4, respectively, and encode the polypeptides having the amino acid sequences shown in SEQ ID NOS. 5, 6, 7, and 8, respectively can be derived from *G. oxydans* strain DSM No. 4025.

The AADHs including Enzymes A, A', A" and B provided by the present invention

20 can be produced from a recombinant organism by any conventional means for expressing, recovering and purifying a recombinant protein. For example, the enzyme can be obtained by culturing the recombinant organism containing the DNA encoding the enzyme so as to produce the enzyme, disrupting the recombinant organism, and isolating and purifying them from cell free extracts of the disrupted recombinant organism, preferably from the

25 soluble fraction of the recombinant organism.

The recombinant organisms provided in the present invention may be cultured in an aqueous medium supplemented with appropriate nutrients under aerobic conditions. The cultivation may be conducted at a pH between about 4.0 and 9.0, preferably between about 6.0 and 8.0. While the cultivation period varies depending upon pH, temperature and
5 nutrient medium used, usually 2 to 5 days will bring about favorable results. A preferred temperature range for carrying out the cultivation is from about 13°C to 45°C preferably from about 18°C to 42°C.

It is usually required that the culture medium contains such nutrients as assimilable
10 carbon sources, digestible nitrogen sources and inorganic substances, vitamins, trace elements and other growth promoting factors. As assimilable carbon sources, glycerol, D-glucose, D-mannitol, D-fructose, D-arabitol, D-sorbitol, L-sorbose, and the like can be used.

15 Various organic or inorganic substances may also be used as nitrogen sources, such as yeast extract, meat extract, peptone, casein, corn steep liquor, urea, amino acids, nitrates, ammonium salts and the like. As inorganic substances, magnesium sulfate, potassium phosphate, ferrous and ferric chlorides, calcium carbonate and the like may be used.

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In the following, the properties of the purified recombinant AADH enzymes specifically from *P. putida* and the production method are summarized.

(1) Enzyme activity

The AADHs of the present invention catalyze oxidation of alcohols and aldehydes including D-sorbitol, L-sorbose, and L-sorbose in the presence of an electron acceptor according to the following reaction formula.

Alcohol+ Electron acceptor \rightarrow Aldehyde + Reduced electron acceptor

Alcohol+ Electron acceptor \rightarrow Ketone + Reduced electron acceptor

Aldehyde + Electron acceptor \rightarrow Carboxylic acid + Reduced acceptor

10 Sugar alcohol + Electron acceptor \rightarrow Aldose + Reduced electron acceptor

Sugar alcohol + Electron acceptor \rightarrow Ketose + Reduced electron acceptor

Aldehyde ketose+Electron acceptor \rightarrow Ketocarboxylic acid+Reduced electron acceptor

Carboxylic acid+Electron acceptor \rightarrow Ketocarboxylic acid+Reduced electron acceptor

15 The enzymes herein do not utilize molecular oxygen as an acceptor. As an acceptor, 2,6-dichlorophenolindophenol (DCIP), phenazine methosulphate (PMS), Wurster's blue, ferricyanide, coenzyme Q or cytochrome c can be used.

The enzymatic activity of the AADHs herein can be determined by methods known in the art, such as by photometric analysis using a spectrophotometer. In accordance with the present invention, one unit of enzyme activity was defined as the amount of enzyme which catalyzed the reduction of 1 μ mole of DCIP per minute. The extinction coefficient of DCIP at pH 8.0 was taken as 15 mM^{-1} . In a preferred standard assay for determining the enzyme activity of the AADHs herein, a first cuvette includes a standard reaction mixture (1.0 ml) containing 0.1 mM DCIP, 1 mM PMS, 2 to 125 mM substrate, 50 mM Tris-malate-NaOH buffer (pH 8.0), and 10 μ l of the enzyme solution. A second cuvette, i.e., a

reference cuvette, contains all the above components except the substrate. The reference cuvette is used to standardize the background absorbance resulting from a substrate-independent (endogenous) reaction. Preferably, a double beam spectrophotometer is used to determine the activity of the enzyme in the presence of a substrate with respect to a standard reaction mixture in the absence of the substrate.

(2) Properties of the AADHs

a) Substrate specificity and products of the enzymatic reaction

The Enzymes A, A', A'' and B were characterized by their substrate specificities as described above using 8 substrates: n-propanol, isopropanol, D-glucose, D-sorbitol, L-sorbose, D-mannitol, L-sorbose, and D-fructose. The results are indicated in Table 1.

Table 1. Substrate specificity of the Enzymes A, A', A'' and B

Substrate	(units/mg of purified protein)			
	Enzyme A	Enzyme A'*	Enzyme A''	Enzyme B
50 mM n-Propanol	139.6	180.7	262.3	40.0
50 mM Isopropanol	76.8	108.9	154.9	72.3
50 mM D-Glucose	2.4	0.0	17.8	943.9
125 mM D-Sorbitol	14.0	7.8	30.1	130.9
2mM L-Sorbose	23.15	5.0	26.5	73.6
50 mM D-Mannitol	7.1	1.3	6.2	517.4
125 mM L-Sorbose	47.4	1.6	30.3	8.4
125 mM D-Fructose	30.7	2.9	17.3	2.1

*: Values of the Enzyme A' was corrected by 1.5-fold, since purity of the enzyme was about 65%.

Enzyme B showed a high reactivity for D-glucose or D-mannitol, but relatively low reactivity for n-propanol and isopropanol. Enzyme A, Enzyme A' and Enzyme A'' showed a high reactivity for n-propanol and isopropanol, but a low reactivity for D-glucose and D-

mannitol; the enzymes showed similar substrate specificity patterns, except that the Enzyme A' had a very low reactivity for L-sorbose or D-fructose.

Products formed from a substrate in the reaction with Enzyme A, Enzyme A', Enzyme A" or Enzyme B were analyzed by thin layer chromatography (TLC) and/or high performance liquid chromatography (HPLC) with authentic compounds. Enzyme A, Enzyme A' and Enzyme A" (designated A group) converted D-sorbitol, L-sorbose, L-sorbose, D-mannitol, and D-fructose to D-glucose with L-gulose, L-sorbose with 2KGA, 2KGA, D-mannose, and 2-keto-D-gluconic acid (2KD), respectively. Enzyme B (designated B group) converted D-glucose, D-sorbitol, L-sorbose, D-mannitol, L-idose, glycerol, D-gluconic acid, D-mannonic acid to D-gluconate, L-sorbose, 2KGA, D-fructose, L-idonic acid, dihydroxyacetone, 5-keto-D-gluconic acid, and 5-keto-D-mannonic acid, respectively. Similarly to the reactivity for L-sorbose, D-glucosone can be converted to 2KD by all of above mentioned AADHs. A group enzymes can produce 2KD from D-fructose whose possible direct product is D-glucosone. All of the enzymes showed the activity for alcohols including sugar alcohol such as D-sorbitol and D-mannitol, and aldehydes including aldose such as D-glucose and ketose such as L-sorbose.

b) Optimum pH

20

All the enzymes have their optimal point at pH 8.0 - 8.5 as shown in Table 2. The Enzymes A" and B have a relatively wide pH range toward a lower pH, compared with the Enzymes A and A'.

Table 2. Optimal pH of the enzymes

pH	(Relative activity, %)			
	Enzyme A	Enzyme A'	Enzyme A''	Enzyme B
6.0	6.5	2.1	35.0	21.0
6.5	13.0	9.3	57.3	51.6
7.0	33.1	22.5	74.8	61.6
7.5	57.7	46.8	90.0	75.3
8.0	100.0	100.0	100.0	100.0
8.5	113.2	142.7	85.6	62.2
9.0	50.0	2.1	46.5	8.0
9.5	19.6	1.8	23.9	0.0

c) pH stability

5

Enzymes A, A', A'' and B were incubated in buffers of various pH-values for 3 hours at 25 °C and the residual activities were assayed and expressed as relative values against that obtained by no incubation at pH 8. Enzymes A, A', A'' and B were stable between pH 6 to 9 as shown in Table 3.

10

Table 3. pH stability of the enzymes

pH	(Relative activity, %)			
	Enzyme A	Enzyme A'	Enzyme A''	Enzyme B
4.0	5.4	0.0	6.2	25.2
5.0	32.0	10.0	77.9	56.1
6.0	74.7	82.7	105.8	100.9
7.0	76.9	96.9	100.9	101.9
8.0	80.1	100.0	99.0	114.0
9.0	60.1	97.3	100.9	101.9
10.0	53.2	85.4	104.0	85.5
11.0	31.0	61.3	79.2	70.1

d) Thermal stability

The residual activities after the treatment of the enzymes at 4, 20, 30, 40, 50, and 60°C for 5 minutes are shown in Table 4.

5

Table 4. Thermal stability of the enzymes

Temperature	(Relative activity, %)			
	Enzyme A	EnzymeA'	Enzyme A''	Enzyme B
4 °C	100.0	100.0	100.0	100.0
20 °C	91.5	100.8	96.0	97.2
30 °C	78.0	103.6	86.1	95.4
40 °C	19.9	78.9	72.8	84.6
50 °C	4.1	0.6	26.6	29.2
60 °C	2.9	0.0	13.3	0.0

e) Effect of metal ions and inhibitors

10

Remaining activities after the treatment of the enzymes with various metals and inhibitors are shown in Table 5. $MgCl_2$ and $CaCl_2$ were nearly inert to the enzymes, while the other metal ions, especially $CuCl_2$, significantly affected the reactivity. EGTA and EDTA inhibited the Enzymes A, A' and A'', remarkably. However, Enzyme B was less

15 inhibited than the A group enzymes by EDTA and EGTA.

Table 5. Effect of metals and inhibitors on activities of the Enzymes A, A', A'' and B.

Compound	(Relative remaining activity)				
	Enzyme	A	A'	A''	B
	Substrate	L-Sorbose	n-Propanol	L-Sorbose	D-Sorbitol
5mM CoCl ₂		16.6	7.9	46.9	23.6
5mM CuCl ₂		0.0	0.0	0.0	0.0
5mM ZnCl ₂		1.5	6.1	19.2	0.0
5mM MgCl ₂		96.3	85.3	78.8	100.0
5mM CaCl ₂		98.8	95.3	123.0	102.9
5mM MnCl ₂		0.0	45.7	0.0	0.0
5mM FeCl ₂		16.6	0.0	0.0	5.9
5mM FeCl ₃		7.8	0.0	44.7	0.0
5mM NiSO ₄		42.7	59.7	90.3	79.4
10mM EDTA		43.1	55.1	52.6	91.3
10mM EGTA		20.4	16.7	56.4	74.0
1mM NaF		98.2	97.1	94.9	100.8
2mM NEM		91.7	97.2	94.9	100.8
1mM ICH ₂ COONa		97.2	78.3	95.3	100.2
0.5mM Hydroxyl-amine-HCl		104.6	98.8	97.2	102.1

f) Molecular weight and subunit

5

Enzymes A, A', A'' and B purified from *P. putida* transconjugants consist of one type of unit with the molecular weight of about 64,000, 62,500, 62,500 and 60,000, respectively, as measured by sodium dodecyl sulfate polyacrylamide gel electrophoresis.

They can be heterodimers consisting of any two units of Enzymes A, A', A'' and B when

10 DNA sequences encoding Enzymes A, A', A'' and B are expressed in the same host.

g) N-terminal amino acid sequence

N-terminal sequences of mature Enzymes A and B are

5 Enzyme A : Gln-Val-Thr-Pro-Val-Thr----

Enzyme A" : Blocked N-terminal residue

Enzyme B : Gln-Val-Thr-Pro-Ile-Thr-Asp-Glu-Leu-Leu-Ala----.

The N-terminus of the mature Enzyme A' is not determined because of an insufficient purity of the sample.

10

(3) Production of the AADHs

Cells are harvested from the fermentation broth by centrifugation or filtration. The cells are suspended in the buffer solution and disrupted by means of a homogenizer,
15 sonicator or treatment with lysozyme and the like to give a disrupted solution of cells.

AADHs are isolated and purified from a cell free extract of disrupted cells, preferably from the soluble fraction of the microorganisms by usual protein purification methods such as ammonium sulfate precipitation, dialysis, ion exchange chromatographies,
20 gel filtration chromatographies, and affinity chromatographies.

(4) Enzyme reaction

Enzyme reaction was performed at pH values from about 6.0 to about 9.0 at the
25 temperature of about 10°C to about 50°C, and preferably about 20°C to 40°C in the presence of an electron acceptor, for example, DCIP, PMS, Wurster's blue, ferricyanide,

coenzyme Q, cytochrome c and the like in a buffer such as Tris-HCl buffer, phosphate buffer and the like. The concentration of the substrate in a reaction mixture can vary depending on the other reaction conditions but, in general, is desirable to be about 1 - 200 g/l, and most preferably from about 1 - 100 g/l.

5

In the enzyme reaction, AADHs may also be used in an immobilized state with an appropriate carrier. Any means of immobilizing enzymes generally known to the art may be used. For instance, the enzyme may be bound directly to membrane granules, or the like, of a resin having functional groups, or it may be bound through bridging compounds
10 having functional groups, for example, glutaraldehyde, to the resin.

The recombinant organisms provided by the present invention are highly useful for the production of the recombinant enzymes having alcohol and aldehyde dehydrogenase activity. Said organisms are also useful for the production of aldehydes, carboxylic acids
15 and ketones, especially, 2KGA by utilizing said recombinant enzymes, and by utilizing the recombinant organisms.

The production of 2KGA can be obtained from the recombinant organisms by fermentation of the recombinant organisms with the medium and culture conditions as
20 described above. The production of 2KGA may be performed with the recombinant organisms described above together with concomitant organisms such as *E. coli*, *P. putida* and *Bacillus megaterium*.

In accordance with the present invention, 2KGA obtained by the methods
25 described herein can be transformed into vitamin C (L-ascorbic acid) by methods known in the art.

Examples

Example 1. Cloning of AADH genes

5 (1) Construction of a genomic library of *G. oxydans* DSM No. 4025

Chromosomal DNA was prepared as follows. *G. oxydans* DSM No. 4025 was cultivated on an agar plate containing 20 ml of NS2 medium consisting of 5.0% D-mannitol, 0.25% MgSO₄·7H₂O, 1.75% corn steep liquor, 5.0% baker's yeast (Oriental Yeast Co., Osaka, Japan), 0.5% CaCO₃, 0.5% urea (sterilized separately) and 2.0% agar (pH 7.0 before sterilization) at 27°C for 3 days. The cells were collected from the agar plate, washed with 10 ml of 10 mM Tris-HCl buffer (pH 8.0) containing 1mM EDTA and resuspended in 5 ml of 10 mM Tris-HCl buffer (pH 8.0) containing 20 mM EDTA. The cell suspension was treated with lysozyme (Sigma Chemicals Co., St. Louis, Mo., USA) at a final concentration of 400 µg/ml at 37°C for 30 minutes, then with pronase (400 units) at 37°C 30 minutes and with 1% SDS at 37°C for 1 hour. Chromosomal DNA was treated with phenol and RNase A (Boehringer Mannheim, GmbH, Mannheim, Germany) according to the method described by Maniatis et al. (Molecular cloning: a laboratory manual. Cold Spring Harbor Laboratory, Cold Spring Harbor, N. Y., (1982).

20 Chromosomal DNA (200 µg) was digested with 168 units of *Sa*II (Boehringer Mannheim) at 37°C for 5 to 90 minutes. The resulting partially digested fragments of 15 - 35 kb were isolated by preparative agarose gel electrophoresis (agarose: 0.7%); the gel piece containing the desired fragments was cut out and the DNAs were electro-eluted from the gel into TAE buffer consisting of 40 mM Tris-acetate and 2 mM EDTA. Thus, 40 µg of the

25 DNAs were obtained. In parallel, 8 µg of the cosmid vector pVK102 (ATCC 37158) was completely digested with *Sa*II and treated with calf intestine alkaline phosphatase

(Boehringer Mannheim) according to the supplier's recommendation. pVK102 (0.4 µg) was ligated with the 15-35 kb *Sa*II fragments (0.2 - 2 µg) by the ligation kit (Takara Shuzo Co. Ltd., Kyoto, Japan) at 26°C for 10 minutes. The ligated DNAs were then used for in vitro packaging according to the method described by the supplier (Amersham): mixing the
5 ligated DNAs with the phage coat protein parts. The resulting phage particles were used to infect *E. coli* ED8767 (Murray, N. E., W. J. Brammar and K. Murray. Mol. Gen. Genet., 150:53-61, 1977). About 3,000 Km^r Tc^s colonies were obtained and all of the colonies tested (24 colonies) possessed the insert DNAs; its average size was 26.5 kb. Another cosmid library of *G. oxydans* DSM No. 4025 containing 55,000 clones was constructed
10 by using chromosomal DNA of *G. oxydans* DSM No. 4025 partially digested with *Eco*RI and inserting them into the *Eco*RI site of pVK100 by almost the same method described above. All of the colonies tested (24 colonies) possessed insert DNAs (average size; 27 kb).

15 These two cosmid libraries in *E. coli* ED8767 were then transferred into *E. coli* S17-1 (Tra⁺, Bio/Technology, 1:784-791, 1983) by using the mixture of recombinant plasmid DNAs extracted from *E. coli* ED8767 libraries. About 4,000 Km^r transformants of *E. coli* S17-1 were picked up, cultivated individually in microtiter plates containing 100 µl of LB consisting of 10 g/l of Bactotrypton (Difco), 5 g/l of yeast extract (Difco) and 5 g/l
20 of NaCl supplemented with 50 µg/ml kanamycin at 37°C, and stocked with 15% glycerol at -80°C as cosmid libraries in *E. coli* S17-1.

 The *G. oxydans* DSM No. 4025-*Sa*II and -*Eco*RI cosmid libraries were constructed in *E. coli* S17-1. From the library, 1,400 clones were individually transferred from *E. coli*
25 S17-1 into *P. putida* ATCC 21812 by conjugal mating. 1,400 cultures stocked in microtiter plates at -80°C were thawed and transferred to microtiter plates containing 100 µl

of fresh LB medium in each well with a plate transfer cartridge (Nunc) and cultivated at 37°C overnight. Nalidixic acid resistant (Nal^r) *P. putida* ATCC21812 was cultivated at 30°C overnight in 100 ml of MB medium consisting of 2.5% mannitol, 0.5% yeast extract (Difco Laboratories, Detroit, Mich.) and 0.3% Bactotryptone (Difco). Fifty µl of the *P.*
5 *putida* culture was individually added to the 1,400 wells containing cultures of the cosmid library. The 1,400 cell mixtures were spotted with plate transfer cartridges onto nitrocellulose filters placed on the surface of FB agar medium consisting of 5% fructose, 1% yeast extract (Difco), 1% polypeptone (Daigo Eiyo, Japan) and 1.8% agar and cultivated at 27°C overnight. Nalidixic acid was used for the counter-selection of
10 transconjugants against donor *E. coli*. The cells grown on the filters were individually streaked onto MB agar medium containing 50 µg/ml of nalidixic acid and 50 µg/ml of kanamycin hereinafter referred to as (MNK agar plate) and incubated for 4 days at 27°C for the selection of transconjugants. The resulting colonies were purified by streaking on MNK agar plates as mentioned above. Thus, 1,400 transconjugants of *P. putida* [gene
15 library of *G. oxydans* DSM No. 4025 in *P. putida*] were prepared.

(2) Immunological screening of clones of the AADH gene of *G. oxydans* DSM No. 4025.

20 At first, 350 transconjugants (175 from *SaI*I library and 175 from *Eco*RI library) maintained MNK agar plates were individually cultivated in test tubes containing 5 ml of MNK medium. The cells were collected from 1.5 ml of each broth and treated for Western-blot analysis as follows. The cells were suspended in 50 µl of Laemmli buffer consisting of 62.5 mM Tris-HCl, pH 6.8, 10% glycerol, 5% mercaptoethanol and 2%
25 SDS. The cell suspension was boiled for 3 minutes, and 10 µl of the cell lysate was applied on SDS-PAGE. The resulting protein bands were then electro-blotted to a

nitrocellulose filter by an electroblotting apparatus (Marysol Industrial Co., Ltd.) operated at 40 V, 200 mA for 16 hours in 2.5 mM Tris-19.2 mM glycine buffer, pH 8.6, containing 20 % methanol. The filter was, then, incubated for 1 hour in 3% gelatin in TBS buffer consisting of 20 mM Tris, pH 7.5, and 500 mM NaCl. After a brief rinse in TTBS buffer consisting of 20 mM Tris, pH 7.5, 500 mM NaCl and 0.05% Tween 20, the filter was incubated for 1 hour with a first-antibody which contained 1:500-diluted anti-AADH antibody in TTBS buffer containing 1% gelatin. The anti-AADH antibody had been prepared by mixing the AADH proteins purified from *G. oxydans* DSM No. 4025 with incomplete adjuvant, injecting the resulting mixture into a white rabbit twice with 2 weeks' interval, collecting whole blood 1 week after the second injection and preparing the serum fraction as the anti-AADH antibody. Then, the filter was washed twice (5 min each) in TTBS buffer and incubated for 1 hour in a second-antibody (goat anti-rabbit IgG-horseradish peroxidase conjugate) solution which contained 1:3,000-diluted second antibody in TTBS containing 1% gelatin. After washing in TTBS buffer twice and in TBS once, the filter was immersed in a color developing solution until blue bands became visible with Konica Immunostaining HRP Kit IS-50B (Konica, Tokyo, Japan) according to the supplier's recommendation. For an actual screening, five cell lysates were mixed and applied to one well for the first Western-blot screening. Out of 70 mixtures, 14 exhibited positive bands; nine samples had immuno-reactive proteins of approximate Mr 64,000, but two of these exhibited weak signals; one had an immuno-reactive protein of approximate Mr 60,000; and four samples had immuno-reactive proteins of Mr 55,000.

Seven mixture samples showing strong signals at Mr 64,000 were individually subjected to a second Western-blot screening to identify the clone in each mixture. One positive clone per one mixture samples was identified; plasmids of the seven clones were designated as p6E10, p16C8, p16F4, p17E8, p1E2, p24D4, and p26C3, respectively. By

restriction enzyme analysis, it was found that four plasmids, p6E10, p16C8, p16F4, and p17E8, carried the same DNA region and the other three carried different regions from that of the former four plasmids.

- 5 (3) Screening of the AADH genes from the cosmid libraries by colony-blot and Southern-blot hybridization

To find the other AADH genes besides the genes obtained by the immunological screening as described above, the whole cosmid libraries of *G. oxydans* DSM No. 4025 in
10 *E. coli* ED 8767 (*SaII*-library and *EcoRI*-libraries) were screened by colony- and Southern-blot hybridization with a 0.9 kb *SaII* fragment of p24D4. The 0.9 kb *SaII* fragment hybridized with a oligonucleotide probe, ATGATGGT(GATC)AC(GATC)AA(TC)GT synthesized according to an internal amino acid sequence of the natural AADH enzyme purified from *G. oxydans* DSM No. 4025,
15 MetMetValThrAsnValAspValGlnMetSerThrGlu, which was obtained by digestion and sequenced by automatic gas-phase sequencer (Applied Biosystems 470A). The cells of the cosmid libraries were appropriately diluted and spread on LK agar plates, and the resulting colonies were blotted onto nylon filters and were analyzed by hybridization with the ³²P-labeled 0.9 kb *SaII* fragment. About 1% of the colonies showed positive signals; 41
20 colonies were selected from the *SaII* library and 20 from *EcoRI* library, and they were subjected to restriction enzyme analysis, followed by Southern-blot analysis. Six different AADH gene-related DNA regions were isolated in this screening as follows: four already-isolated regions carried on p24D4, p1E2, p26C3 and, p17E8, and two new regions carried on two separate plasmids designated as pSS31 and pSS53. The other plasmid pSS33
25 carried both of the two regions which were carried on p24D4 and pSS31.

(4) Immunological and enzymatic characterization of AADH clones

Western-blot analysis of cell lysates of *P. putida* carrying p24D4, p1E2, p26C3, pSS31 and p17E8 showed that the five clones encoded proteins with molecular weights of about 64,000, 62,500, 62,500, 60,000 and 62,000, respectively. Plasmid pSS33 encoded two immuno-reactive proteins with molecular weights of about 64,000 and 60,000, whereas pSS53 did not produce any immuno-reactive proteins.

Enzyme activities of each clone (cell free extract, soluble fraction and membrane fraction) were measured by photometric analysis. The cells of each clone were inoculated in 5 ml of MB medium in a test tube and cultivated at 30°C for 24 hours. The resulting broth was transferred into 200ml of fresh MB medium in 500 ml flask and the flask was shaken on the rotary flask shaker at 30°C for 24 hours. The cells were collected by centrifugation at 6,000 x g for 10 minutes and washed with 40 ml of cold buffer consisting of 50 mM Tris-HCl, pH 7.5, 5mM MgCl₂ and 0.5 mM phenylmethylsulfonyl fluoride and suspended with the same buffer to prepare cell suspension of 1 g wet cells per 5ml. The cell suspension was subjected twice to a French press cell disruptor (1,500 kg/cm²) and the resulting homogenate was centrifuged at 6,000 x g for 10 minutes to remove cell debris. Thus obtained cell free extract (CFE) was centrifuged at 100,000 x g for 60 minutes. The resulting supernatant and pellet were collected as the cytosol fraction and the membrane fraction, respectively and subjected to PMS-DCIP assay as follows. The enzyme reaction mixture (1.0 ml) contained 100 µM DCIP, 1mM PMS, 50 mM Tris malate-NaOH buffer, pH 8.0, a substrate and the enzyme (10 µl). Substrate-dependent decreasing rate of absorbance of DCIP at 600 nm was measured at 25°C by using a Kontron spectrophotometer UVIKON 810. Table 6 shows the level of enzyme activities in the cell free extract and the soluble fractions of the clones. According to the substrate specificity,

the enzyme encoded on each plasmid was classified into large three groups, A-, B- and C- groups: A-group catalyzes the oxidation of L-sorbose, D-sorbitol and 1-propanol; B-group catalyzes the oxidation of D-glucose and D-sorbitol; C-group showed no clearly detectable activities on the substrates used. In the A-group, there were three types, A, A' and A" each of which was distinguished from each other by their physical map of the DNA carried on each plasmid. B- or C-group each consisted of only one type of protein derived from one region of the chromosomal DNA.

Table 6.

Enzyme Group	Enzyme Name	Plasmid	Soluble fraction					
			CFE					
			Sorbose 125 mM	Sorbose*1 125 mM	Glucose*2 50 mM	Sorbitol*3 125 mM	Sorbose*4 2 mM	n-Propanol 50 mM
A	A	p24D4	+++	+++	-	+++	+++	++++
A	A'	p1E2	+	+	-	+	+	+
A	A"	p26C3	+	+	-	+/-	+	+
B	B	pSS31	-	-	++++	++	+	+
C	-	p17E8	-	-	+/-	-	-	-
A and B	A and B	pSS33	+++	+++	++++	++++	+++	++++
10	Level of the activity;			++++	:	very high		
				+++	:	high		
				++	:	medium		
				+	:	low		
				+/-	:	trace		
15				-	:	not detected		

*1 - *4: Oxidation product of each substrate was determined by a resting cell reaction followed by TLC analysis.

- 20 *1: Oxidation product of L-sorbose by Enzymes A, A', A", and [A and B] was 2KGA.
 *2: Oxidation product of D-glucose by Enzyme B, and Enzyems [A and B] was D-gluconic acid.
 *3: Oxidation product of D-sorbitol by Enzymes A, A', and A" was mainly D-glucose; that by Enzyme B was L-sorbose; and that by Enzymes [A and B] was mixture of D-glucose and L-sorbose.
 25 *4: Oxidation product of L-sorbose by Enzymes A, A', A", B, and [A and B] was 2KGA.

Example 2. Nucleotide sequencing

Nucleotide sequences of the genes for Enzymes A, A', A'' and B were determined with the plasmids, p24D4, p1E2, p26C3, and pSS31, respectively, by the
5 dideoxynucleotide chain termination method using M13mp18 and M13mp19 (Boehringer Mannheim). One open reading frame (ORF) for each gene was found; the nucleotide sequences of the four genes are shown in the sequence list SEQ ID NOS. 1 to 4 and the amino acid sequences deduced from the nucleotide sequences were shown in the sequence
list SEQ ID NOS. 5 to 8. The ORFs for Enzymes A, A', A'' and B genes are 1737, 1737,
10 1734, and 1737-bp long and encode 579, 579, 578 and 579 amino acid residues all including 23 amino acid of signal sequences.

The homologies between Enzymes A, A', A'' and B are shown in Table 7.

Table 7. Homologies of amino acid sequences among AADHs.

15

	(%)			
	Enzyme A	Enzyme A'	Enzyme A''	Enzyme B
Enzyme A	100	-	-	-
Enzyme A'	89	100	-	-
Enzyme A''	85	86	100	-
Enzyme B	83	82	81	100

Figure 5 shows the amino acid sequences of mature Enzyme A and Enzyme B which are aligned so as to be comparable.

20 Homology search of Enzymes A, A', A'' and B revealed that Enzymes A, A', A'' and B showed rather low homology (26 - 31% homology through the polypeptides) with several quino-proteins including alcohol dehydrogenase of *Acetobacter aceti* (T. Inoue et al., J. Bacteriol. 171: 3115-3122) or *Acetobacter polyoxogenes* (T. Tamaki et al., B. B. A.,

1088:292-300), and methanol dehydrogenase of *Paracoccus denitrificans* (N. Harms et al., J. Bacteriol., 169: 3966-3975), *Methylobacterium organophilum* (S. M. Machlin et al., J. Bacteriol., 170: 4739-4747), or *Methylobacterium extorquens* (D. J. Anderson et al., Gene 90: 171-176).

5

Example 3. Subcloning of AADH genes

Enzyme A gene was originally cloned as a cosmid clone of p24D4 which has about 25 kb insert in *EcoRI* site of pVK100. Then, it was further subcloned to use as an Enzyme
10 A gene cassette. The 2.7 kb *EcoRV* fragment which includes ORF of Enzyme A gene with about 500 bp of non-coding regions at the both ends was excised from 3.4 kb *NruI* fragment, which was isolated from p24D4 in M13 mp18, and was ligated to *HindIII* site of pUC18 with *HindIII* linker (CAAGCTTG). The resulting plasmid was designated pSSA202. Enzyme A gene cassette (2.7kb *HindIII* fragment) was then inserted at *HindIII*
15 site of pVK102 to produce pSSA102R. The plasmid pSSA102R was introduced into nalidixic acid resistant *P. putida* [ATCC 21812] by a conjugal mating method as described in Example 1-(1). The transconjugant of *P. putida* carrying pSSA102R was selected on MB agar medium containing 50 µg/ml nalidixic acid and 10 µg/ml tetracycline (MNT agar medium) and subjected to a mini-resting cell reaction. The reaction mixture (100 µl)
20 consisting of 20 g/l L-sorbose, 3 g/l NaCl, 10 g/l CaCO₃ and the cells collected from the MNT agar culture with a toothpick was incubated at room temperature with gentle shaking for 24 hours. The reaction mixture was assayed with TLC and 2KGA was identified as the product, while no 2KGA was observed by the same resting cell reaction with the host, nalidixic acid resistant *P. putida* [ATCC 21812].

25

Enzyme B gene was originally cloned as a cosmid clone of pSS31 which has about 30kb insert in *SalI* site of pVK102. It was subcloned as 6.5kb *BglII* fragment into *BglII*

site of pVK101 (ATCC 37157) to obtain pSSB102. Then, it was further subcloned to use as a Enzyme B gene cassette. The 6.5 kb *Bgl*III fragment was cloned into *Bam*HI site of pUC18 to obtain pSSB202. Then, 2.3 kb *Xho*II fragment was excised from pSSB202. The 2.3 kb *Xho*II fragment includes ORF of Enzyme B with 120 bp of 5'-noncoding
5 region and about 500 bp of 3'-noncoding region. The fragment was treated with Klenow fragment to fill-in the cohesive ends and cloned into *Hind*III site of pUC18 with *Hind*III linker to produce pSSB203. The Enzyme B gene cassette (2.3 kb *Hind*III fragment) was inserted at *Hind*III site of pVK102 to make pSSB103R. The plasmid pSSB103R was introduced into nalidixic acid resistant *P. putida* [ATCC 21812] by a conjugal mating
10 method, and the transconjugant of *P. putida* carrying pSSB103R was selected on MNT agar medium and subjected to a mini-resting cell reaction. *P. putida* carrying pSSB103R showed the Enzyme B activity (L-sorbose formation from D-sorbitol) in the resting cell reaction. (Incidentally, *Xho*II fragment was found not to be a *Xho*II-*Xho*II fragment, but a *Xho*II-*Xho*I fragment as a result of nucleotide sequencing. *Xho*I might be present in the
15 *Xho*II preparation.)

Enzyme A' and Enzyme A" genes were originally cloned as a cosmid clone of p1E2 and p26C3 which have about 30 kb insert in *Sal*I site of pVK102 and further subcloned basically as described above. Enzyme A' gene in 3.5 kb *Xho*II fragment was subcloned in
20 *Bgl*III site of pVK102 to construct pSSA'101R, and Enzyme A" gene in 2.7 kb *Eco*RV fragment was first subcloned into M13mp19 and then re-subcloned between *Hind*III and *Bgl*III sites of pVK102 to construct pSSA"102.

Example 4. Isolation and characterization of AADHs from transconjugants of *P. putida*.

(1) Cultivation of microorganisms

5 *P. putida* [ATCC 21812] carrying cosmid vector pVK102 containing the Enzyme A, A', A'' and B genes; pSSA102R, p1E2, p26C3 and pSSB103R, respectively, were cultivated in MB broth in the presence of antibiotic. Antibiotics added into medium were as follows; 5 µg/ml tetracycline for pSSA102R (Enzyme A) and pSSB103R (Enzyme B), 25 µg/ml kanamycin for p1E2 (Enzyme A') and p26C3 (Enzyme A''). From the agar plate of
10 MB containing the respective antibiotic, the cells were inoculated in 10 test tubes containing 5 ml MB medium with the respective antibiotic and cultivated with shaking at 30°C. After 2 days of cultivation, the cells were transferred to ten 500 ml-Erlenmeyer flasks containing 100 ml of the same medium and cultivated with shaking at 30°C. After 1 day of cultivation, the seed cultures were combined and transferred to 18 liters of the medium in 30 L jar
15 fermenter (Marubishi) and cultivated for 18 hours with 300 rpm agitation and 1.0 vvm aeration at 30°C. The cells were harvested by centrifuge at 6,000 x g for 10 minutes, washed once with 1.5 liters of 25 mM Tris-HCl, pH 7.5, containing 5 mM CaCl₂, 1 mM MgCl₂, 0.2 M NaCl, 2.5% sucrose, and 0.5 mM PMSF and stocked at -20°C until use. As a result, about 150 g wet weight cells were obtained.

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(2) Purification of the cloned Enzymes A, A', A'', and B.

Purifications of the Enzymes A, A', A'' and B were carried out by the same procedure with almost the same scale. All operations were carried out at 4 - 10°C unless
25 otherwise stated. The enzyme activity determination for Enzyme A, A', A'' and B were carried out with the substrates, L-sorbose, n-propanol, n-propanol and D-glucose,

respectively, by spectrophotometric assay as described in Example 1 throughout the purification steps. The cells (about 100 g wet weight cells containing 8 - 10 g of total proteins) were thawed and suspended in about 200 ml of 25 mM Tris-HCl, pH 8.0, and disrupted by passing through French press (1500 kg/cm²) twice. Then, DNase and MgCl₂ were added to the suspension at the final concentration of 0.01 mg/ml and 1 mM, respectively, to reduce viscosity of the solution due to DNA. Cell debris was removed by centrifugation at 6,000 x g for 10 minutes. The suspension was filled up to 240 ml with the 25 mM Tris-HCl buffer, pH 8.0, and centrifuged at 100,000 x g for 90 minutes to remove insoluble membrane fraction. The soluble supernatant was filled up to 240 ml with the Tris buffer and, then, pyrroloquinoline quinone (PQQ) and CaCl₂ were added at the final concentration of 12.5 µM and 5 mM, respectively, and the solution was stirred vigorously for 15 minutes at room temperature. The soluble fraction prepared as above was fractionated by (NH₄)₂SO₄. The fraction 35 - 60%-saturated (NH₄)₂SO₄ was precipitated and resuspended in 100 ml of 25 mM Tris-HCl buffer, pH 8.0, containing 5 mM CaCl₂, and 5% sucrose and, then, PQQ was added again at the final concentration of 12.5 µM. The enzyme solution was dialyzed against 1000 ml of the same buffer (without PQQ) overnight. Twenty grams of solid polyethylene glycol #6000 was added to the dialysate slowly with gentle stirring. After stirring for 30 minutes, precipitates were removed by centrifugation at 10,000 x g for 20 minutes, and the supernatant was filled up to 200 ml with the buffer indicated as above.

The enzyme solution prepared as above was purified by following three chromatography steps.

The first step: DEAE-Toyopearl 650M

The crude enzyme solution was subjected to a column of DEAE-Toyopearl 650M (2.5x 40 cm) which had been equilibrated with 25 mM Tris-HCl buffer, pH 8.0, containing 5 mM CaCl₂, and 5% sucrose. The column was washed with 400 ml of the same buffer and the enzyme was eluted by 2,000 ml of 0 - 0.5 M NaCl linear gradient in the buffer at a flow rate of 150 ml/hour. The enzyme active fractions were pooled and diluted 2-fold with the buffer without NaCl.

10 The second step: Q-Sepharose (Fast Flow)

The enzyme solution was subjected to a column of Q-Sepharose (Fast Flow) (1.5 x 20 cm) which had been equilibrated with the buffer without NaCl. The column was washed with 200 ml of the buffer containing 0.2 M NaCl and the enzyme was eluted by 600 ml of 0.2 - 0.6 M NaCl linear gradient in the buffer at a flow rate of 50 ml/hour. The enzyme active fractions were pooled and concentrated to 2.5 ml by using ultrafilter: Amicon, PM-30 under N₂ gas.

The third step: Sephacryl S-300 HR (gel filtration)

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The concentrated enzyme was filtrated by a column of Sephacryl S-300 HR (2.5 x 100 cm) which had been equilibrated with 25 mM HEPES, pH 7.5, containing 5 mM CaCl₂, 5% sucrose, and 0.2 M NaCl. The column was developed by the same buffer at a flow rate of 20 ml/hour. The enzyme active fractions were pooled and concentrated to below 1 ml by the ultrafilter mentioned above and, then, stocked at -80°C. The enzymes concentrated in the HEPES buffer was stable for at least 2 months at -80°C.

Consequently, 26.0 mg of Enzyme A, 0.35 mg of Enzyme A', 0.41 mg of Enzyme A'', and 5.0 mg of Enzyme B were obtained.

(3) Properties of the Enzymes A, A', A'' and B.

5

a) Molecular weight and subunit.

The Enzymes A, A', A'' and B were eluted at the same position from the same gel filtration column on Sephacryl S-300HR under the same condition. The molecular weight of the enzymes was estimated as approximately 135,000 comparing with the molecular weight standard proteins (SDS-PAGE Standards, Low Range, Bio-Rad Laboratories, Richmond, CA, USA). The Enzymes A, A', A'' and B showed homogeneous single bands on SDS-PAGE analysis with molecular weights of 64,000, 62,500, 62,500 and 60,000, respectively. All the Enzyme bands A, A', A'' and B were detected on Western blotting analysis using anti-AADH rabbit serum. Therefore, it was concluded that the enzymes consisted of two identical subunits as an homo-dimeric form.

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b) N-terminal amino acid sequence and amino acid composition.

20 N-terminal amino acid sequences of the mature Enzymes A, A'' and B were analyzed with automatic gas-phase sequencer (470A; Applied Biosystems) by Edman method [Acta Chem. Scand., 4, 283-293, {1950}]. The analysis of the Enzyme A' was not done because of an insufficient purity of the sample. The results were as follows:

Enzyme A : Gln-Val-Thr-Pro-Val-Thr----

25 Enzyme A'' : Blocked N-terminal residue

Enzyme B : Gln-Val-Thr-Pro-Ile-Thr-Asp-Glu-Leu-Leu-Ala-----.

The determined sequences of Enzyme A and B were identical to the sequences (starting from the twenty-fourth residues) deduced from the nucleotide sequences described in SEQ ID NOS. 5 and 8; these results indicate that the initial 23 residues of the enzymes are the signal sequences. By analogy of the Enzymes A and B, the first 23 residues of Enzyme A' and A'' are also deduced to be the signal sequences.

The amino acid composition of the Enzyme A was determined. The protein was hydrolyzed with 6 N HCl at 110°C for 24 hours or 4 M methanesulfonic acid (after oxidation with performic acid) at 115°C for 24 hours. Amino acid analysis was performed by using Kontron amino acid analyzer (ninhydrin system). The analytical data were compared with the amino acid composition deduced from the DNA sequence of Enzyme A gene. It indicated that the purified Enzyme A was certainly a product of the Enzyme A gene.

15 c) Substrate specificity

The Enzymes A, A', A'' and B were characterized by their substrate specificities on PMS-DCIP assay as described above using 8 substrates, n-propanol, isopropanol, D-glucose, D-sorbitol, L-sorbose, D-mannitol, L-sorbose, and D-fructose. The results were indicated in Table 1.

d) Physicochemical property

Physicochemical studies of optimal pH, pH stability and thermal-stability, of the Enzymes A (as L-sorbose dehydrogenase activity), A' (as n-propanol dehydrogenase

activity), A" (as L-sorbose dehydrogenase activity) and B (as D-sorbitol dehydrogenase activity), were performed by the PMS-DCIP assay.

Table 2 summarizes the results of optimal pH of the enzymes. The enzyme activity
5 was assayed by the PMS-DCIP spectrophotometric assay using various pH buffers. The buffers were 50 mM Tris-malate-NaOH, pH 6.0, 6.5, 7.0, 7.5, 8.0 and 8.5; 50 mM glycine-NaOH, pH 9.0 and 9.5. The extinction coefficients of DCIP at pH 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0 and 9.5 were taken as 10.8, 13.2, 14.5, 14.9, 15.0, 15.1, 15.1 and 15.1, respectively. All the enzymes showed their optimal points at pH 8.0 - 8.5. The
10 Enzymes A" and B had relatively wide pH range toward lower pH, compared with the Enzymes A and A'.

Table 3 indicates the results of pH-stabilities of the enzymes. The enzyme (about 0.01 mg/ml) was incubated with 50 mM buffer containing 5% sucrose, 0.2 M NaCl, and
15 5mM CaCl₂ at 25°C for 3 hours and assayed by PMS-DCIP spectrophotometric method. The buffers were Na-acetate, pH4 and 5, Tris-malate-NaOH, pH 6, 7 and 8, glycine-NaOH, pH 9 and 10. The values in the table are expressed as relative activity against that obtained by no incubation at pH 8.0. The substrates used for the enzymes were 125mM L-sorbose for Enzymes A and A", 50 mM n-propanol for Enzyme A', and 125 mM D-sorbitol for Enzyme B. Profiles of pH-stabilities of Enzymes A, A', A", and B were
20 almost the same; they were stable at the range of pH 6 to 9.

Table 4 indicates the results of thermal-stabilities of the enzymes. The enzyme (about 0.05 mg/ml) in 25 mM HEPES buffer, pH 7.5, containing 5% sucrose, 0.2M
25 NaCl, and 5 mM CaCl₂ was incubated at temperature indicated in the table (4 - 60°C) for 5 minutes, cooled in ice bath and assayed by PMS-DCIP spectrophotometric method.

Remaining activity was expressed as relative activity against that obtained by 4°C incubation. The substrates used for the enzymes were 125mM L-sorbose for Enzyme A and Enzyme A", 50 mM n-propanol for Enzyme A', and 125 mM D-sorbitol for Enzyme B. After the treatment of the enzymes at 40°C for 5 min, the residual activity of Enzyme A was 20%, and those of Enzymes A', A", and B were 70 - 85%.

e) General inhibitors

The enzyme (about 0.05 mg/ml) in 25 mM HEPES buffer, pH 7.5, containing 5% sucrose was incubated with metal or inhibitor for 30 minutes at 25°C. Remaining activity was assayed by PMS-DCIP spectrophotometric assay as described in Example 1. Remaining activity is expressed as relative activity against blank incubation. Effects of metal ions on the enzymes are listed in Table 5. MgCl₂ and CaCl₂ were nearly inert to the enzymes, while the other metal ions, especially CuCl₂, significantly affected. Effects of inhibitors on the enzymes are also included in Table 5. EGTA and EDTA inhibited the Enzyme A, A' and A", remarkably. However, Enzyme B was less inhibited than the A group enzymes by EDTA and EGTA.

Example 5. Efficient production of Enzyme B in *E. coli*

The signal peptide region of the Enzyme B was replaced with that of maltose binding protein (malE) of *E. coli* as follows. Two oligonucleotides (SEQ ID NOS. 9 and 10) were synthesized with Applied Biosystem 381A DNA synthesizer and annealed to generate a double-stranded DNA fragment encoding a amino acid sequence (SEQ ID NO. 11), MetLysIleLysThrGlyAlaArgIleLeuAlaLeuSerAlaLeuThrThrMetMetPheSer

AlaSerAlaLeuAla(Gln), which was, then, treated with T4 polynucleotide kinase [J. Biol. Chem., 259, 10606-10613, (1984)]. pSSB203 (see Example 3) was digested with the restriction enzyme *SphI*, treated with T4 DNA polymerase and digested with *BstP1*. The resulting 1.72 kb DNA fragment carrying Enzyme B gene without the region coding for the original signal sequence and the first amino acid residue (Gln) of the mature Enzyme B was isolated from an agarose gel after agarose gel electrophoresis. The *E. coli* expression vector, pTrc99A (Pharmacia Co., Uppsala, Sweden), which was digested with the restriction enzymes *NcoI* (at ATG start codon) and *SmaI* was ligated with above two DNA fragments. The resulting plasmid was designated as pTrcMal-EnzB and used to transform *E. coli* JM109. The transformant was grown in two 2-liter flasks each containing 600 ml of LB with 100 µg/ml ampicillin at 28°C and IPTG was added to 0.1 mM when cell concentration reached at about 1.5 OD600. Following the addition of IPTG, the cells were cultivated for an additional 3 - 4 hours. The cells were harvested by centrifugation (4,000 x g) at 25°C for 10 minutes, suspended with 500 ml of 30 mM Tris-HCl, pH 8.0, containing 20% sucrose at 25°C. After EDTA was added to 1 mM into the cell suspension, the cells were incubated with gentle shaking for 5 minutes at 25°C and collected by centrifugation (8,000 x g) at 4°C for 15 minutes. The cells were resuspended with 500 ml of ice cold 5 mM MgSO₄ solution and incubated with gentle shaking for 5 minutes at 4°C. The cell suspension was centrifuged at 8,000 x g for 10 minutes at 4°C to obtain a supernatant as a cold osmotic shock extract, which was found to contain the Enzyme B protein (a molecular weight of 60,000) with the purity more than 50 - 60% by SDS-PAGE analysis. The supernatant was first supplemented with Tris-HCl, pH 8.0, to 20 mM, and incubated at 25°C firstly with EDTA at 10 mM final concentration for 10 min, secondly with CaCl₂ at 20 mM final concentration for 10 minutes and lastly with PQQ at 25 µM final concentration. For stabilization of the enzyme, α-methyl-D-glucoside (a competitive inhibitor) was added to 20 mM final concentration in the supernatant. The Enzyme B was

completely purified by following two chromatographies. At first, the supernatant was loaded onto a Q-Sepharose column (1.6 x 12 cm) which had been equilibrated with 20 mM Tris-HCl, pH 8.0, containing 1 mM CaCl₂ and 20 mM α -methyl-D-glucoside, and the Enzyme B was eluted with 600 ml of 0 - 0.4 M NaCl linear gradient in the same buffer. A red protein peak eluted at about 0.25 M NaCl was collected and concentrated to about 0.5 ml by Centricon-30 (Amicon). Finally, the Enzyme B was passed through a SephacrylS-300HR column with 20 mM HEPES, pH 7.8, containing 0.2 M NaCl, 1 mM CaCl₂ and 20 mM α -methyl-D-glucoside. A red protein peak eluted around a molecular weight of 135,000 daltons position was collected as the final purified Enzyme B. Consequently, about 8 mg of the purified Enzyme B was obtained from 1.2 liters cultivation broth of *E. coli*.

Example 6. Host-vector system

A host-vector system for *G. oxydans* [DSM No. 4025] was established by using the conjugal mating system with a broad-host-range cosmid, pVK102. Initially, only one transconjugant was isolated from *G. oxydans* [DSM No. 4025] having nalidixic acid resistance. A new host, GOS2, was isolated from the transconjugants, *G. oxydans* [DSM No. 4025] carrying pVK102 by curing pVK102. A second host, GOS2R, was then derived from the GOS2 by adding rifampicin resistance (100 μ g/ml), which enables easy selection of the transconjugants from the donor *E. coli*. The plasmid transfer frequency into GOS2R was $10^{-3} \sim 10^{-4}$ transconjugants/recipient. The 2KGA productivity of GOS2R, however, was about 10% lower than that of *G. oxydans* [DSM No. 4025]. The third host, GORS6-35, was obtained from *G. oxydans* [DSM No. 4025] by selecting the strain with rifampicin resistance, high 2KGA productivity and relatively high competence through a series of experiments, including the conjugation, curing and 2KGA fermentation.

(1) Isolation of GOS2

Resistance to nalidixic acid was added to *G. oxydans* [DSM No. 4025]. Cells of *G. oxydans* [DSM No. 4025] were streaked onto Trypticase Soy Broth (BBL, Becton Dickinson Microbiology Systems Cockeysville, MD. USA) (T) agar medium with 50 µg/ml of nalidixic acid (TN agar medium) and incubated at 27°C for 5 days. The resulting colonies were again streaked on the same agar plates to obtain a nalidixic acid-resistant *G. oxydans* DSM No. 4025, GON. The broad-host-range cosmid pVK102 (Km^r, Tc^r) was transferred from *E. coli* carrying pVK102 into the GON strain by the tri-parental conjugal mating as follows. A helper strain, *E. coli* carrying pRK2013 and a donor strain carrying pVK102 were cultivated in LB medium with 50 µg/ml of kanamycin at 37°C overnight. The cultures were transferred to fresh LB medium with kanamycin and incubated for 5-6 hours. Recipient strain, GON, was cultivated in TN liquid medium at 30°C overnight. *E. coli* and GON strains were separately centrifuged and re-suspended in equal- and one tenth- volume of fresh T medium, respectively. One hundred µl of each cell suspension was mixed together and 30 µl portion of the mixture was spotted onto a nitrocellulose filter placed on the surface of a NS2 agar plate. Transconjugants were selected on the T agar medium containing 50 µg/ml of nalidixic acid and 50 µg/ml of kanamycin (TNK agar medium). Several colonies were obtained on the selection plates where many spontaneous mutants of *E. coli* (Nal^r, Km^r) colonies also appeared. The plasmid and chromosomal DNAs of the transconjugant candidates were prepared and compared with the authentic pVK102 and chromosomal DNA of *G. oxydans* DSM No. 4025 by restriction analysis and Southern-blot hybridization. Consequently, one transconjugant of *G. oxydans* [DSM No. 4025] carrying pVK102, GON8-1, was identified. The plasmid DNA prepared from GON8-1 was identical to that of pVK102 and replicable in *E. coli*. The chromosomal DNA of GON8-1 was identical to that of *G. oxydans* [DSM No. 4025].

To isolate strains that could work as hosts with higher competence for conjugal mating, the transconjugant GON8-1 was cured of the plasmid pVK102. GON8-1 was cultivated in T broth without antibiotics at 30°C for 2 days, 2% of the culture was transferred into fresh T broth. After three such cultivation cycles, the cells were spread on
5 T agar plates, incubated at 27°C for 4 days, and the resulting colonies were picked onto TNK and TN agar plates to select Km^S strains. One of the Km^S strains was designated as GOS2 and was confirmed by Southern-blot hybridization not to be carrying any DNA region of pVK102. Then, pVK102 was transferred into strain GOS2 by a conjugal mating; this strain showed 10² ~ 10³ fold higher competence (namely 10⁻⁵ ~ 10⁻⁶ transconjugants
10 / recipient) than *G. oxydans* [DSM No. 4025] did.

(2) Isolation of GOS2R, a rifampicin-resistant mutant of GOS2.

Rifampicin resistant (Rif^r) mutants from GOS2 were isolated through repeated
15 transfer of GOS2 cells onto T agar medium containing 20 ~ 100 µg/ml rifampicin; one of the Rif^r strains was designated as GOS2R. Strain GOS2R showed very high competence; 10⁻² ~ 10⁻³ and 10⁻⁴ transconjugants /recipient on TRK agar (T agar medium containing 100 µg/ml rifampicin and 50 µg/ml kanamycin) plate and on TRT agar (T agar medium containing 100 µg/ml rifampicin and 3 µg/ml tetracycline) plate, respectively.

20

2KGA productivity from L-sorbose by GOS2R was compared with that of *G. oxydans* [DSM No. 4025]. The cells maintained on NS2 agar medium were inoculated into 5 ml of the seed culture medium consisting of 8% L-sorbose (sterilized separately), 0.05% glycerol, 0.25% MgSO₄·7H₂O, 1.75% corn steep liquor, 5.0% baker's yeast,
25 1.5% CaCO₃, and 0.5% urea (sterilized separately) (pH 7.0 before sterilization) and incubated at 30°C for 24 hours. The resulting seed culture (5 ml) was inoculated into a

500-ml Erlenmeyer flask containing 50 ml of the production medium PMS10 consisting of 10% L-sorbose, (sterilized separately), 0.05% glycerol, 0.25% $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 3% corn steep liquor, 6.25% baker's yeast, 1.5% CaCO_3 , and 1.6% urea (sterilized separately) (pH 7.5 before sterilization) and incubated at 30°C for 4 days with shaking (180 rpm). The quantitative determination of 2KGA was assayed by high performance liquid chromatography. GOS2R and *G. oxydans* [DSM No. 4025] produced 87.3 and 97.3 g/l of 2KGA, respectively.

(3) Isolation of GORS6-35 as a host with high 2KGA productivity

To evaluate the self-cloning of AADH genes in the strain with the same productivity of 2KGA from L-sorbose as *G. oxydans* [DSM No. 4025], a new host was constructed by (i) adding rifampicin-resistance (200 $\mu\text{g/ml}$), (ii) introducing and curing pVK102, and (iii) selecting 2KGA high producer from L-sorbose. Thus obtained GORS6-35 shows the following two characteristics: (i) almost the same 2KGA productivity (about 100 g/l 2KGA from 10% L-sorbose) as the parent *G. oxydans* [DSM No. 4025]; and (ii) a competence ($10^{-6} \sim 10^{-7}$ transconjugants /recipient).

Example 7. Construction of promoter-replaced Enzyme B gene.

The promoter of Enzyme A gene (PA) is likely strong in *G. oxydans* [DSM No. 4025] because Enzyme A was found to be one of the highest-expressing proteins in amount in the cell when total cell free extract of *G. oxydans* [DSM No. 4025] was subjected to SDS-polyacrylamide gel electrophoresis and the resulting gel was stained with Coomassie Brilliant Blue R-250. The PA and another promoter, a promoter of kanamycin resistant gene of Tn5 (PTn5), which could express the kanamycin resistance in *G. oxydans* [DSM

No. 4025], were attached to the structure gene with the SD sequence of Enzyme B gene as shown in Fig. 10.

Enzyme B gene-containing 2.3 kb *Hind*III fragment was inserted in M13 mp18 and the resulting phage DNA was subjected to site-directed mutagenesis carried out with T7-GENTM In Vitro Mutagenesis Kit (TOYOBO Co., Ltd., Osaka Japan) according to the recommendations by the supplier (Fig. 9). To insert various promoters upstream of Enzyme B gene instead of Enzyme B promoter, *Bam*HI site was created upstream of the SD sequence. A primer for the mutagenesis, GTTAGCGCGGTGGATCCCCATTGGAGG (27-mer including *Bam*HI site, SEQ-IDNo. 12), were synthesized with Applied Biosystems 381A DNA synthesizer. The resulting *Bam*HI-*Hind*III fragment carries Enzyme B SD and structural genes without the Enzyme B promoter (PB).

Then promoter of Enzyme A gene (PA) was subcloned by PCR method using primers tagged with the sequences for the *Hind*III and *Bam*HI sites. The PCR reaction was carried out with GeneAmpTM DNA Amplification Reagent Kit (Takara Shuzo, Kyoto, Japan) with a thermal cycler, Zymoreactor II (Atto Corp., Tokyo, Japan). The reaction consists of pre-treatment before adding enzyme (94°C, 5 minutes.); 30 cycles of denaturation step (94°C, 1 minute.), annealing step (60°C, 1 minute.), and synthesis step (72°C, 1 minute.); and post-treatment (72°C, 5 minutes.). Plasmid pSSA202 (pUC18-Enzyme A gene in 2.7kb *Hind*III) was used as the template DNA. The reaction mixture contained 200 µM of dNTPs, 1 µM of each primer, 1 ng of template DNA and 2.5 u of AmpliTaqTM DNA polymerase in the buffer supplied. Consequently, 300 bp fragment upstream from the SD sequence was amplified. The PCR product was inserted into

pUC18 between *Hind*III and *Bam*HI sites and used for nucleotide sequencing; the amplified sequences do not have any mutations caused by misincorporation in PCR.

The promoter of the kanamycin resistant gene, PTn5, was first obtained as a
5 *Hind*III-*Pst*I fragment from the plasmid pNeo (Pharmacia Co., Uppsala, Sweden). The *Hind*III-*Pst*I fragment was then inserted into the multicloning site of pUC18, and finally the PTn5 was excised as a *Hind*III-*Bam*HI fragment.

The *Hind*III-*Bam*HI fragments containing the PA and PTn5 promoters were
10 inserted in the *Hind*III site of pUC18 together with *Bam*HI-*Hind*III fragment containing the PB promoter-removed Enzyme B structural gene. The *Hind*III fragments from the resulting plasmids were subcloned into pVK100 to produce pSSAP-B and pSSPTn5-B, which were transferred into GOS2R by conjugal mating as described in Example 6.

15 Example 8. 2KGA production by transconjugants of GOS2R in flask

(1) 2KGA production from L-sorbose by Enzyme-A gene-amplified transconjugant in single culture fermentation in flask.

20 The Enzyme A plasmid, pSSA102R, and the vector plasmid, pVK102, were introduced into GOS2R by a conjugal mating method as described in Example 6. The resulting transconjugants were maintained on NS2 agar medium containing 30 µg/ml tetracycline and subjected to 2KGA fermentation from L-sorbose. The cells of the transconjugants were inoculated into 5 ml of the seed culture medium described in Example
25 6 and incubated at 30°C for 24 hours. The resulting seed culture (5 ml) was inoculated into a 500-ml Erlenmeyer flask containing 50 ml of the PMS10 production medium described in

Example 6 or the PMS12 production medium consisting of 12% L-sorbose, (sterilized separately), 0.05% glycerol, 0.25% $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 3% corn steep liquor, 10 % baker's yeast, 1.5% CaCO_3 , and 2% urea (sterilized separately) (pH 7.5 before sterilization) and incubated at 30°C for 4 or 5 days with shaking (180 rpm). As a result, GOS2R

- 5 (pSSA102R) and GOS2R (pVK102) produced 92.2 and 89.1 g/l 2KGA , respectively, from 10% L-sorbose in 4 days, and 105.7 and 99.9 g/l 2KGA, respectively, from 12% L-sorbose in 5 days.

- (2) 2KGA production from D-sorbitol by GOS2R (pSSB103R) in single culture
10 fermentation in flask.

The Enzyme B plasmid, pSSB103R, and the vector plasmid, pVK102, were introduced into GOS2R by a conjugal mating method as described in Example 6. The resulting transconjugants were maintained on NS2 agar medium containing 30 µg/ml
15 tetracycline and subjected to 2KGA fermentation from D-sorbitol. The cells of the transconjugants were inoculated into 5 ml of the seed culture medium consisting of 8% D-sorbitol, 0.05% glycerol, 0.25% $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 1.75% corn steep liquor, 5.0% baker's yeast, 1.5% CaCO_3 , and 0.5% urea (sterilized separately) (pH 7.0 before sterilization) and incubated at 30°C for 24 hours. The resulting seed culture (5 ml) was inoculated into a
20 500-ml Erlenmeyer flask containing 50 ml of three production media shown in Table 8 and incubated at 30°C for 3 days with shaking (180 rpm). As a result, GOS2R (pSSB103R) produced about 61.5, 71.5 and 73.0 g/l of 2KGA from 8%, 10% and 12% D-sorbitol, respectively, while GOS2R (pVK102) produced 19.5, 25.4 and 30.2 g/l 2KGA, respectively.

25

Ingredients	PMSL8	PMSL10	PMSL12
D-Sorbitol	8.0	10.0	12.0
Glycerol	0.05	0.05	0.05
MgSO ₄ ·7H ₂ O	0.25	0.25	0.25
CSL	3.0	3.0	3.0
Baker's yeast	5.0	6.25	10
Urea*	1.25	1.6	2.0
CaCO ₃	1.5	1.5	1.5

pH 7.5 before sterilization

*: sterilized separately

- 5 (3) 2KGA production from D-sorbitol by GOS2R (pSSAP-B) and GOS2R (pSSPTn5-B) in single culture fermentation in flask.

The cells of GOS2R (pSSAP-B), GOS2R (pSSPTn5-B) and GOS2R (pSSB103R), GOS2R (pVK100) were cultivated in the PMSL10 production medium in Erlenmeyer flasks at 30°C for 3 days as described in Example 8 (2). The amounts of 2KGA produced were shown in Table 9.

Strain	1 day	2 days	3 days
GOS2R (pSSAP-B)	47.2	67.0	67.7
GOS2R (pSSPTn5-B)	23.4	28.6	29.4
GOS2R (pSSB103R)	30.5	54.3	62.7
GOS2R (pVK100)	10.2	18.3	19.3
GOS2R	6.7	14.7	16.4

Example 9 2KGA production from D-sorbitol in 3-L Jar fermentations by single microorganism

(1) Single culture fermentation by GOS2R (pSSB103R)

5

Five ml portions of the seed culture prepared in test tubes as described in Example 8-(2) were transferred to four 500-ml Erlenmeyer flasks containing 50 ml of the same seed culture medium and incubated at 30°C for 24 hours with shaking (180 rpm). The resulting broth (200 ml of the seed culture) was inoculated into 3-L jar fermentor containing 1800 ml of the PMSL10 production medium containing 3ml of antifoam. The fermentor was operated at 30°C, 700 rpm and 0.5vvm. D-Sorbitol was fed in ways: (i) 200 ml of 50% D-sorbitol was fed in 6 hours from the 24th to the 30th hour; or (ii) 280 ml of 50% D-sorbitol was fed in 8.3 hours from the 24th to the 32.3th hour. As a result, 99.0 and 103.4 g/l 2KGA were produced by the fed-batch fermentations (i) and (ii), respectively in 51 hours.

15

Example 10. 2KGA production from D-sorbitol by Enzyme B gene-amplified GOS2R in mixed culture fermentation with *E. coli* in flask

(1) Mixed-culture fermentations with *B. megaterium*, *E. coli* and *P. putida*.

20

B. megaterium [DSM No. 4026], *E. coli* HB101 and *P. putida* [ATCC 21812], growth factor suppliers, were cultivated in 150 ml of the seed culture medium consisting of 0.3% yeast extract (Difco), 0.3% beef extract (Kyokuto Seiyaku, Tokyo, Japan), 3% corn steep liquor, 1% polypeptone (Kyokuto), 0.1% urea, 0.1% KH₂PO₄, 0.02% MgSO₄·7H₂O, 2% L-sorbose, 0.1% CaCO₃ (pH 7.1 before sterilization) for 24 hours at 37, 37, and 30°C, respectively. Strain GOS2R (pSSB103R) was cultivated in two test tubes containing 5 ml of the seed culture medium as described in Example 8-(2) at 30°C for

25

24 hours. Four ml of GOS2R (pSSB103R) seed cultures and 3.5 ml of growth factor supplier seed culture were inoculated to a 500-ml of Erlenmeyer-flask containing 50 ml of the production medium for mixed culture fermentations consisting of 8% D-sorbitol, 0.01% $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 1% corn steep liquor, 0.1% KH_2PO_4 , 0.6% CaCO_3 , 1.5% urea (sterilized separately) and antifoam (one drop per flask) (pH 7.0 before sterilization) and the flask was shaken at 30°C for 46.5 hours. As a result, mixed culture with *B. megaterium* DSM No. 4026, *E. coli* HB101 and *P. putida* ATCC 21812 produced 49.9, 54.1, 31.3 g/l 2KGA, respectively.

10 (2) Mixed culture fermentation of GOS2R (pSSAP-B) with *E. coli* in flask.

Mixed culture fermentations by GOS2R (pSSAP-B) with *E. coli* was performed in the same manner as described above except for the seed culture medium for *E. coli* containing 2% D-sorbitol instead of 2% L-sorbose. From 10% of D-sorbitol, GOS2R (pSSAP-B) produced 73.7 g/l 2KGA in 48.5 hours.

Example 11. 2KGA production by recombinant AADH

A reaction mixture containing 1.7 mg/ml of purified Enzyme A (purified according to Example 4), 50 mM Tris-HCl, pH 7.5, 5 mM CaCl_2 , 8 mg/ml bovine serum albumine (BSA), 1mM PMS, 20 µg/ml PQQ, and 4% L-sorbose was incubated at 30°C with gentle shaking for 20 hours. As a result, about 2 g/l 2KGA (TLC assay) was produced.

The other reaction mixture containing 2.4 mg/ml each of purified Enzyme A and Enzyme B (purified according to Example 4), 50 mM Tris-HCl, pH7.5, 5 mM CaCl_2 , 8 mg/ml BSA, 1mM PMS, 20 µg/ml PQQ, and 2% D-sorbitol was incubated at 30°C with

gentle shaking for 20 hours. As a result, 0.25 g/l 2KGA (HPLC assay) and about 5 g/l L-sorbose (TLC assay) were produced.

Example 12. Production of aldehydes from alcohols, ketones from alcohols or carboxylic acids and carboxylic acids from aldehydes.

Enzyme reactions with purified Enzyme A or Enzyme B and various substrates were performed as described in Example 11. The resulting products were identified by TLC and/or HPLC as shown in Table 10.

10 Table 10

Enzyme	Substrate	Product
Enzyme A	D-Sorbitol	D-Glucose, L-Gulose
	L-Sorbose	L-Sorbose, 2KGA
	L-Sorbose	2KGA
	D-Mannitol	D-Mannose
	D-Fructose	2KD
Enzyme B	D-Glucose	D-Gluconic acid
	D-Sorbitol	L-Sorbose
	L-Sorbose	2KGA
	D-Mannitol	D-Fructose
	L-Idose	L-Idonic acid
	Glycerol	Dihydroxyacetone
	D-Gluconic acid	5-Keto-D-gluconic acid
	D-Mannonic acid	5-Keto-D-mannonic acid

Enzyme A converted D-fructose to 2KD; this means that D-glucosone was also a product formed from D-fructose as the intermediate.

Example 13. 2KGA and L-sorbose production by a transconjugant of *P. putida*

A resting cell mixture (2 ml) containing 1% CaCO₃, 0.3% NaCl, 1mM PMS, 5 µg/ml PQQ, 2% L-sorbose and 10 OD600 unit-cells of nalidixic acid resistant (Nal^r) *P. putida* [ATCC 21812] carrying pSSA102R or pVK100 was incubated at 30°C with gentle shaking for 17 hours. As a result, Nal^r *P. putida* [ATCC 21812] carrying pSSA102R or pVK100 produced 18.9 or 0.0 g/l of 2KGA, respectively.

A resting cell mixture (2 ml) containing 1% CaCO₃, 0.3% NaCl, 1mM PMS, 5 µg/ml PQQ, 2% D-sorbitol and 10 OD600 unit-cells of Nal^r *P. putida* [ATCC 21812] with pSSB103R or with pVK100 was incubated at 30°C with gentle shaking for 17 hours. As a result, Nal^r *P. putida* [ATCC 21812] carrying pSSB103R or with pVK100 produced 7.8 or 0.0 g/l of L-sorbose, respectively.

Example 14. Construction and characterization of chimera AADH enzymes

(1) Construction of chimera AADH enzymes

To alternate substrate specificity of AADH enzymes, a variety of chimera enzymes between Enzymes A and B were constructed.

(i) Figure 2 shows the structure of the chimera genes by strategy I (restriction and ligation method). The restriction sites conserved in both genes, *Ava* I (nucleotide No. 603 of Enzyme A gene), *Eco*RI site (nucleotide No. 1084), and *Sa*I site (nucleotide No. 1470) (Fig. 7) were used for the construction. First, Enzyme A and B gene cassettes (2.7 kb and 2.3 kb Hind III fragments, respectively) were subcloned in the same direction in this order

on pUC18 to produce the plasmid pSSAB201, and Enzyme B and A gene cassettes were also subcloned in the same direction in this order on pUC18 to produce pSSBA201 (Fig. 3). After partial digestion of these plasmids with each restriction enzyme, resulting digests were ligated and used to transform *E. coli* JM109. Ampicillin resistant transformants were analyzed for their plasmids, and Enzyme A gene-headed and Enzyme B-headed chimera gene cassettes with the expected *Hind*III fragment size of 2.7 kb and 2.3 kb, respectively, were selected. Thus constructed chimera gene cassettes were introduced into *Hind*III site of pVK102 to produce pSSA/B101R, pSSA/B102R, pSSA/B103R, pSSB/A101R, pSSB/A102R, and pSSB/A103R which encode Enzyme A/B1, EnzymeA/B2, EnzymeA/B3, EnzymeB/A1, EnzymeB/A2, and EnzymeB/A3, respectively, as shown in Fig. 2. These six plasmids were introduced into NaI^r *P. putida* by a conjugal mating method as described in Example 1.

(ii) Figure 8 shows the scheme for constructing chimera genes by strategy II; in vivo homologous recombination method to construct chimeras recombined at random positions for altering the substrate specificity of AADH enzymes. The principle of this method is as follows: (i) Locate two homologous genes to be recombined tandem in one plasmid with selective marker; (ii) Cut it at restriction sites between the two genes, and transform *rec A*⁺ *E. coli* cell with the linearized plasmid; (iii) Select transformants showing selective marker which carry circularized DNAs by recombination between the two genes at various positions. Two plasmids pSSAB201 and pSSBA201 which have Enzyme A and Enzyme B genes on pUC18 (Fig. 3) were linearized with pairs of restriction enzymes as shown in Fig. 8. *E. coli* JM101(*rec A*⁺) was transformed with these linearized DNAs. Transformants were obtained at frequency of 10¹-10² /μg DNA. To begin with, DNA size was determined to remove illegitimate recombinants. As a result, correct recombinants were obtained at ratio of 30%. *Xho*I-*Bal*I fragment in which Enzyme A gene lost about

two-third of C-terminus was efficient to obtain chimeras recombined within one-third of N-terminus. Next, the recombinants were classified into recombination site groups bordered by restriction sites of three *Sma*I, *Sph*I, *Sal*I and *Bal*I (Fig. 7). Thus constructed chimera genes were subcloned on pVK100 as *Hind*III cassette and the plasmids were introduced into *Nal*^r *P. putida* by a conjugal mating method.

(2) Characterization of chimera AADH enzymes

(i) Characteristics of the chimeras obtained by restriction and ligation method

The chimera enzymes expressed in *Nal*^r *P. putida* were characterized enzymatically by using soluble fractions of the cells of the transconjugants as described in Example 1. Eight substrates were used for the evaluation as shown in Fig. 11. Enzymes A/B1 and A/B3 showed Enzyme A-type substrate specificity, although their expression level was lower than that of Enzyme A. On the other hand, Enzymes B/A1, B/A2, and B/A3 showed Enzyme B-type substrate specificity, although activity on n-propanol (Enzyme A type activity) became higher in accordance with the increase of the region from Enzyme A; the expression level of Enzyme B/A1 gene was about 2-fold higher than that of wild Enzyme B gene. As a result from the chimeras obtained by recombination and ligation method, it was concluded that the N-terminal one third region of Enzyme A or Enzyme B primarily determines its substrate specificity.

(ii) Characteristics of the chimeras obtained by homologous recombination method.

Among the chimeras obtained as above, seven out of eighteen chimera enzymes obtained from the chimera genes recombined between *Sma*I2 and *Sal*I sites illustrated in Fig. 7 showed preferable substrate specificity. The seven chimera enzymes converted D-

sorbitol to L-sorbose, not to D-glucose produced by Enzyme A, and converted L-sorbose to 2KGA like Enzyme A. The recombination sites were determined by nucleotide sequencing as described in Example 2. These type of chimeras have an approximate structure of " N-terminal 2/9 of Enzyme A + C-terminal 7/9 of Enzyme B " was classified as Enzyme superA-type. There were three Enzyme superA-type enzymes according to the recombined site: Enzyme A/B21(chimera consisting of Enzyme A amino acid residue Nos. 1 - 128 and Enzyme B amino acid residue Nos. 129 - 556), Enzyme A/B22 (chimera consisting of Enzyme A amino acid residue Nos. 1 - 125 and Enzyme B amino acid residue Nos. 126- 556) and Enzyme A/B25 (chimera consisting of Enzyme A amino acid residue Nos. 1 - 135 and Enzyme B amino acid residue Nos. 136 - 556). *P. putida* transconjugant expressing genes of Enzyme A/B21, Enzyme A/B22 or Enzyme A/B25 converted D-sorbitol to L-sorbose and did not convert D-sorbitol to D-glucose. The other type of chimera Enzyme A/B31 (Enzyme A amino acid residue Nos. 1 - 95 and Enzyme B amino acid residue Nos. 96 - 556) converted D-sorbitol to L-sorbose efficiently and did not convert L-sorbose to 2KGA; this chimera showed Enzyme B-type activity. Expression level of above mentioned chimeras was higher than that of wild Enzyme B because it was found that the Enzyme B gene contains many rare codons but Enzyme A does not when the genes were analyzed with the program, Codon Preference (Wisconsin Sequence Analysis PackageTM, Genetics Computer Group).

(3) Improvement of codon usage in chimera genes

To further improve the chimeras, Enzyme A/B21, Enzyme A/B22, Enzyme A/B25 and Enzyme A/B31 in the view point of the preferable codon usage, the C-terminal two thirds consisting of Enzyme B residues were replaced with the C-terminal two thirds consisting of Enzyme A residues. Enzyme A/B21, Enzyme A/B22, Enzyme A/B25 and Enzyme A/B31 genes were used for constructing new chimera genes of Enzyme sA21 (Enzyme A amino acid residue Nos. 1 - 128, Enzyme B amino acid residue Nos. 129 - 180 and Enzyme A amino acid residue Nos. 180 - 556), Enzyme sA22 (Enzyme A amino acid residue Nos. 1 - 125, Enzyme B amino acid residue Nos. 126 - 180 and Enzyme A amino acid residue Nos. 180 - 556), Enzyme sA2 (Enzyme A amino acid residue Nos. 1 - 135, Enzyme B amino acid residue Nos. 136 - 180 and Enzyme A amino acid residue Nos. 180 - 556) and Enzyme sB (Enzyme A amino acid residue Nos. 1 - 95, Enzyme B amino acid residue Nos. 96 - 180 and Enzyme A amino acid residue Nos. 180 - 556) (Fig. 4).

Actually, the replacement experiments for Enzyme sA2 and Enzyme sB were performed by partially digesting the plasmids, pUC18 carrying Enzyme sA gene and Enzyme B/A1 gene and pUC 18 carrying Enzyme A/B31 gene and Enzyme B/A1 gene with *Ava*I, ligating the resulting digests, transforming *E. coli* JM109, analyzing the plasmid structure of the transformants by restriction analysis, and determining the nucleotide sequence to confirm the expected recombination site, *Ava*I. The replacement experiments for Enzyme sA21 and Enzyme sA22 were performed by replacing the *Hind*III-*Ssp*I fragment of pSSsA2 encoding N-terminal part of Enzyme sA2 with the corresponding *Hind*III-*Ssp*I fragment containing recombinated site of Enzyme A/B21 or Enzyme A/B22 gene (Fig. 4).

(4) Kinetic properties of chimera enzymes

Tables 11 and 12 summarize the kinetic properties of chimera enzymes, Enzyme sA2 and Enzyme sB in comparison with Enzyme A and Enzyme B, respectively.

5

Table 11. Enzyme sA2 vs Enzyme A

	Enzyme sA2	Enzyme A
$K_{msorbose}$	128 mM	36 mM
$K_{msorbitol}$	2140	388
$K_{mglucose}$	20	-

Products from L-sorbose in product assay with Enzyme sA2 and Enzyme A were 2KGA. Products from D-sorbitol in product assay with Enzyme sA2 and Enzyme A were L-sorbose with trace amount of D-glucose and D-glucose only, respectively. Thus, Enzyme sA2 showed desired characteristics for 2KGA production from D-sorbitol; L-sorbose/L-sorbose dehydrogenase activity to produce 2KGA from L-sorbose like Enzyme A and D-sorbitol dehydrogenase activity to produce L-sorbose from D-sorbitol like Enzyme B.

10

Table 12. Enzyme sB vs Enzyme B

	Enzyme sB	Enzyme B
$K_{msorbitol}$	61 mM	128 mM
$K_{isorbose}$	150	100

15

In comparison with Enzyme B, Enzyme sB showed higher affinity to D-sorbitol and lower affinity to L-sorbose which is the oxidation product of D-sorbitol and inhibitor in the conversion of D-sorbitol to L-sorbose.

Example 15. 2KGA production from D-sorbitol by GOS2R derivative strain amplified with chimera AADH enzymes

For evaluating Enzyme sA2 and Enzyme sB, GOBΔK and GOI13 strains were
5 constructed. GOBΔK was made from GOS2R by deleting the whole Enzyme B gene and instead inserting 1.28 kb Km^r gene cassette isolated from pUC4K [4.1 kb, Km^r, Amp^r; Pharmacia, Uppsala, Sweden; Viera, J., and Messing, J., Gene 19:259, (1982)] by using a suicide vector pSUP201 [Amp^r, Cm^r, mob⁺, a derivative of pBR325, Bio/Technology, 1:784-791, (1983)].

10

GOI13 was constructed from GOBΔK by replacing wild Enzyme A gene with Enzyme sB gene and deleting wild Enzyme A" gene replaced with gentamicin (Gm) resistant gene cassette with the suicide vector pSUP202 [Amp^r, Cm^r, Tc^r, mob⁺, a derivative of pBR325, Bio/Technology, 1:784-791, (1983)]. The Gm^r gene cassette was
15 designed to have *Pst*I site at both ends by PCR amplification with the DNA fragment Tn5-GM [Sasagawa et al., Gene 56: 283-288, (1987)] as the template, and the resulting PCR product was inserted into *Pst*I site of pUC4K to produce pUC8G; Gm^r gene can be isolated from pUC8G by digesting with *Eco*RI, *Bam*HI, *Sal*I, or *Pst*I.

20 (1) Effect of Enzyme sA2 amplification in 2KGA production

Plasmid pSSsA2, pVK100 with 2.7 kb *Hind*III cassette containing Enzyme sA2 gene, and its control plasmid pSSA102R, pVK102 with 2.7 kb *Hind*III cassette containing Enzyme A gene, were introduced into GOI13 by a conjugal mating method as described in
25 Example 6. The resulting transconjugants were cultivated in PMSL10 medium at 30°C for 4 days as described in Example 8. GOI13 carrying pSSsA2 and pSSA102R produced

66.3 and 38.5 g/l of 2KGA, respectively, and 8.4 and 25.9 g/l of 2KD (by-product of 2KGA produced from D-sorbitol via D-glucose and D-gluconate), respectively.

(2) Plasmids pSSsA21 and pSSsA22, which are pVK100 with 2.7 kb *HindIII* cassettes containing Enzyme sA21 and Enzyme sA22 genes, respectively(Fig. 4), were introduced into GOI13 by a conjugal mating method as described in Example 6. The resulting transconjugants were cultivated in PMSL10 medium at at 30°C for 4 days as described in Example 8. GOI13 carrying pSSsA21 and pSSsA22 produced 66.8 and 77.4 g/l of 2KGA, respectively, and 0.3 and 0.4 g/l of 2KD, respectively.

10

(3) Effect of Enzyme sB in 2KGA production

Plasmid pSSsB, pVK100 with 2.7 kb *HindIII* cassette containing Enzyme sB gene (Fig. 4) and its control plasmid pSSB103R, pVK102 containing 2.3 kb Enzyme B gene, were introduced into GOBAK by a conjugal mating method. GOBAK carrying pSSsB, GOBAK carrying pSSB103R, and GOBAK were cultivated in PMSL8 medium as described in Example 8 (2) and produced 52.0, 46.8, and 1.1 g/l of 2KGA, respectively, and 6.9, 9.3, 32.3 g/l of 2KD, respectively.

20 GOI13, which carries one copy of Enzyme sB on the chromosomal DNA without wild genes of Enzyme B, Enzyme A, and Enzyme A", was also cultivated in PMSL10 medium in 2 days . It produced 79.3 g/l of L-sorbose.

The terms and expressions which have been employed and used herein are terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions

thereof; it being recognized that various modifications are possible within the scope of the invention.

SEQUENCE LISTING

5 (1) GENERAL INFORMATION

(i) APPLICANT

NAME: F. HOFFMANN-LA ROCHE AG

STREET: Grenzacherstrasse 124

10 CITY: Basle

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15 TELEX: 962292/965542 hlr c

(ii) TITLE OF INVENTION:

Novel Alcohol/Aldehyde Dehydrogenases

(iii) NUMBER OF SEQUENCES: 12

(iv) COMPUTER READABLE FORM:

20 (A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: Macintosh

(C) OPERATING SYSTEM:

(D) SOFTWARE: MS word ver 5.1

25

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1740 base pairs

(B) TYPE: nucleic acid

5 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter oxydans*

10 STRAIN: DSM 4025

(iv) FEATURE:

FEATURE KEY: CDS

POSITION: 1..1737

15 SEQUENCING METHOD: E

ATGAAACCGA CTTGCTGCT TTGGGCCAGT GCTGGCGCAC TTGCATTGCT 50
20 TGCCGCACCC GCCTTTGCTC AAGTGACCCC CGTCACCGAT GAATTGCTGG 100
CGAACCCGCC CGCTGGTGAA TGGATCAGCT ACGGTCAGAA CCAAGAAAAC 150
25 TACCGTCACT CGCCCCTGAC GCAGATCACG ACTGAGAACG TCGGCCAACT 200
GCAACTGGTC TGGGCGCGCG GCATGCAGCC GGGCAAAGTC CAAGTCACGC 250
CCCTGATCCA TGACGGCGTC ATGTATCTGG CAAACCCGGG CGACGTGATC 300
30 CAGGCCATCG ACGCCAAAAC TGGCGATCTG ATCTGGGAAC ACCGCCGCCA 350
ACTGCCGAAC ATCGCCACGC TGAACAGCTT TGGCGAGCCG ACCCGCGGCA 400
TGGCGCTGTA CGGCACCAAC GTTTACTTTG TTTCGTGGGA CAACCACCTG 450
35 GTCGCCCTCG ACACCGCAAC TGGCCAAGTG ACGTTCGACG TCGACCGCGG 500
CCAAGGCGAA GACATGGTTT CGAACTCGTC GGGCCCGATC GTGGCAAACG 550

	GCGTGATCGT	TGCCGGTTCG	ACCTGCCAAT	ACTCGCCGTT	CGGCTGCTTT	600
5	GTCTCGGGCC	ACGACTCGGC	CACCGGTGAA	GAGCTGTGGC	GCAACTACTT	650
	CATCCCGCGC	GCTGGCGAAG	AGGGTGATGA	GACTTGGGGC	AACGATTACG	700
	AAGCCCGTTG	GATGACCGGT	GCCTGGGGCC	AGATCACCTA	TGACCCCGTC	750
10	ACCAACCTTG	TCCACTACGG	CTCGACCGCT	GTGGGTCCGG	CGTCGGAAAC	800
	CCAACGCGGC	ACCCCGGGCG	GCACGCTGTA	CGGCACGAAC	ACCCGTTTCG	850
15	CGGTGCGTCC	TGACACGGGC	GAGATTGTCT	GGCGTCACCA	GACCCTGCCC	900
	CGCGACAAC	GGGACCAGGA	ATGCACGTTC	GAGATGATGG	TCACCAATGT	950
	GGATGTCCAA	CCCTCGACCG	AGATGGAAGG	TCTGCAGTCG	ATCAACCCGA	1000
20	ACGCCGCAAC	TGGCGAGCGT	CGCGTGCTGA	CCGGCGTTCC	GTGCAAAACC	1050
	GGCACCATGT	GGCAGTTCGA	CGCCGAAACC	GGCGAATTCC	TGTGGGCCCCG	1100
25	TGATACCAAC	TACCAGAACA	TGATCGAATC	CATCGACGAA	AACGGCATCG	1150
	TGACCGTGAA	CGAAGATGCG	ATCCTGAAGG	AACTGGATGT	TGAATATGAC	1200
	GTCTGCCCCG	CCTTCTTGGG	CGGCCGCGAC	TGGCCGTCCG	CCGCACTGAA	1250
30	CCCCGACAGC	GGCATCTACT	TCATCCCGCT	GAACAACGTC	TGCTATGACA	1300
	TGATGGCCGT	CGATCAGGAA	TTCACCTCGA	TGGACGTCTA	TAACACCAGC	1350
35	AACGTGACCA	AGCTGCCGCC	CGGCAAGGAT	ATGATCGGTC	GTATTGACGC	1400
	GATCGACATC	AGCACGGGTC	GTACGCTGTG	GTCGGTCGAA	CGTGCTGCGG	1450
	CGAACTATTC	GCCCGTCTTG	TCGACCGGCG	GCGGCGTTCT	GTTCAACGGT	1500
40	GGTACGGATC	GTTACTTCCG	CGCCCTCAGC	CAAGAAACCG	GCGAGACCCT	1550
	GTGGCAGACC	CGCCTTGCAA	CCGTGCGGTC	GGGCCAGGCC	ATCTCTTACG	1600
45	AGGTTGACGG	CATGCAATAT	GTCGCCATCG	CAGGTGGTGG	TGTCAGCTAT	1650
	GGCTCGGGCC	TGAACTCGGC	ACTGGCTGGC	GAGCGAGTCG	ACTCGACCGC	1700
	CATCGGTAAC	GCCGTCTACG	TCTTCGCCCT	GCCGCAATAA		1740

INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1740 base pairs

(B) TYPE: nucleic acid

5 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter oxydans*

10 STRAIN: DSM 4025

(iv) FEATURE:

FEATURED KEY: CDS

POSITION: 1..1737

SEQUENCING METHOD: E

15

	ATGAAGACGT	CGTCTTTGCT	GGTTGCGAGC	GTTGCCGCGC	TTGCAAGCTA	50
20	TAGCTCCTTT	GCGCTTGCTC	AAGTGACCCC	CGTCACCGAT	GAATTGCTGG	100
	CGAACCCGCC	CGCTGGTGAA	TGGATCAGCT	ACGGTCAGAA	CCAAGAAAAC	150
	TACCGTCACT	CGCCCCTGAC	GCAGATCAGC	ACTGAGAACG	TCGGCCAACT	200
25	GCAACTGGTC	TGGGCGCGCG	GCATGCAGCC	GGGCAAAGTC	CAAGTCACGC	250
	CCCTGATCCA	TGACGGCGTC	ATGTATCTGG	CAAACCCGGG	CGACGTGATC	300
30	CAGGCCATCG	ACGCCAAAAC	TGGCGATCTG	ATCTGGGAAC	ACCGCCGCCA	350
	ACTGCCGAAC	ATCGCCACGC	TGAACAGCTT	TGGCGAGCCG	ACCGCGGGCA	400
	TGGCGCTGTA	CGGCACCAAC	GTTTACTTTG	TTTCGTGGGA	CAACCACCTG	450
35	GTCGCCCTCG	ACACCGCAAC	TGGCCAAGTG	ACGTTGACG	TCGACCGCGG	500
	CCAAGGCGAA	GACATGGTTT	CGAACTCGTC	GGGCCCCGATC	GTGGCAAACG	550

	GCGTGATCGT	TGCCGGTTCG	ACCTGCCAAT	ACTCGCCGTT	CGGCTGCTTT	600
5	GTCTCGGGCC	ACGACTCGGC	CACCGGTGAA	GAGCTGTGGC	GCAACTACTT	650
	CATCCCGCGC	GCTGGCGAAG	AGGGTGATGA	GACTTGGGGC	AACGATTACG	700
	AAGCCCGTTG	GATGACCGGC	GTCTGGGGTC	AGATCACCTA	TGACCCCGTT	750
10	GGCGGCCTTG	TCCACTACGG	CTCGTCGGCT	GTTGGCCCGG	CTTCGGAAAC	800
	CCAGCGCGGC	ACCACCGGCG	GCACCATGTA	CGGCACCAAC	ACCCGTTTTCG	850
15	CTGTCCGTCC	CGAGACTGGC	GAGATCGTCT	GGCGTCACCA	AACTCTGCCC	900
	CGCGACAAC	GGGACCAAGA	GTGCACCTTC	GAGATGATGG	TTGCCAACGT	950
	TGACGTGCAG	CCCGCAGCTG	ACATGGACGG	CGTCCGCTCG	ATCAACCCGA	1000
20	ACGCCGCCAC	CGGCGAGCGT	CGCGTTCTGA	CCGGCGTTCC	GTGCAAAACC	1050
	GGCACCATGT	GGCAGTTCGA	CGCCGAAACC	GGCGAATTCC	TGTGGGCCCCG	1100
25	TGACACCAGC	TACGAGAACA	TCATCGAATC	GATCGACGAA	AACGGCATCG	1150
	TGACCGTCGA	CGAGTCGAAA	GTTCTGACCG	AGCTGGACAC	CCCCTATGAC	1200
	GTCTGCCCCG	TGCTGCTGGG	TGGCCGTGAC	TGGCCGTGGG	CTGCGCTGAA	1250
30	CCCCGATACC	GGCATCTACT	TTATCCCGCT	GAACAACACC	TGCATGGATA	1300
	TCGAAGCTGT	CGACCAGGAA	TTCAGCTCGC	TGGACGTGTA	CAACCAAAGC	1350
35	CTGACCGCCA	AAATGGCACC	GGGTAAAGAG	CTGGTTGGCC	GTATCGACGC	1400
	CATCGACATC	AGCACAGGCC	GCACCCTGTG	GACCGCTGAG	CGCGAAGCCT	1450
	CGAACTACGC	GCCTGTCCTG	TCGACCGCTG	GCGGCGTTCT	GTTCAACGGC	1500
40	GGCACCGACC	GTTACTTCCG	CGCTCTCAGC	CAAGAGACCG	GCGAGACCCT	1550
	GTGGCAGACC	CGTCTGGCGA	CTGTCGCTTC	GGGCCAAGCT	GTCTCGTACG	1600
45	AGATCGACGG	CGTCCAATAC	ATCGCCATCG	GCGGCGGCGG	CACGACCTAT	1650
	GGTTCGTTCC	ACAACCGTCC	CCTGGCCGAG	CCGGTCGACT	CGACCGCGAT	1700
	CGGTAATGCG	ATGTACGTCT	TCGCGCTGCC	CCAGCAATAA		1740
50						

INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1737 base pairs

5 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ORIGINAL SOURCE:

10 ORGANISM: *Gluconobacter oxydans*

STRAIN: DSM 4025

(iv) FEATURE:

FEATURE KEY: CDS

POSITION: 1..1734

15 SEQUENCING METHOD: E

20 ATGAAACTGA CGACCCTGCT GCAAAGCAGC GCCGCCCTGC TTGTGCTTGG 50
CACCATTCCC GCCCTTGCCC AAACCGCCAT CACCGATGAA ATGCTGGCGA 100
ACCCGCCCCGCG TGGTGAATGG ATCAACTACG GTCAGAACCA AGAGAACTAC 150
25 CGCCACTCGC CCCTGACGCA GATTACCGCA GACAACGTCG GCCAACTGCA 200
ACTGGTCTGG GCGCGCGGTA TGGAAGCGGG CAAGATCCAA GTGACCCCGC 250
TTGTCCATGA CGGCGTCATG TATCTGGCAA ACCCCGGTGA CGTGATCCAG 300
30 GCCATCGACG CCGCGACCGG CGATCTGATC TGGGAACACC GCCGCCAACT 350
GCCGAACATC GCCACGCTGA ACAGCTTTGG TGAGCCGACC CGCGGCATGG 400
35 CCCTCTATGG CACCAACGTC TATTTCGTCT CGTGGGACAA CCACTTGGTC 450
GCGCTGGACA CCTCGACCGG CCAAGTCGTA TTCGACGTCG ATCGCGGTCA 500

	AGGCACGGAT ATGGTCTCGA ACTCGTCCGG CCCGATTGTC GCCAATGGCG	550
5	TCATCGTTGC GGGCTCGACC TGTCAGTATT CGCCGTTTCGG CTGTTTCGTT	600
	TCGGGCCACG ACTCGGCCAC CGGTGAAGAG CTGTGGCGCA ACAACTTTAT	650
	CCCGCGCGCC GGCGAAGAGG GTGATGAGAC CTGGGGCAAT GATTACGAGG	700
10	CCCGCTGGAT GACCGGCGTT TGGGGCCAGA TCACCTATGA CCCCGTTGGC	750
	GGCCTTGTC ACTACGGCAC CTCAGCAGTT GGCCCTGCGG CCGAGATTCA	800
15	GCGCGGCACC GTTGGCGGCT CGATGTATGG CACCAACACC CGCTTTGCTG	850
	TCCGCCCCGA GACCGGCGAG ATCGTCTGGC GTCACCAAAC TCTGCCCCGC	900
	GACAACTGGG ACCAAGAGTG TACGTTTCGAG ATGATGGTCG TCAACGTCGA	950
20	CGTCCAGCCC TCGGCTGAGA TGGAAGGCCT GCACGCCATC AACCCCGATG	1000
	CCGCCACGGG CGAGCGTCGC GTTGTGACCG GCGTTCCGTG CAAGAACGGC	1050
25	ACCATGTGGC AGTTCGACGC CGAAACCGGC GAATTCCTGT GGGCGCGCGA	1100
	CACCAGCTAT CAGAACCTGA TCGAAAGCGT CGATCCCGAT GGTCTGGTGC	1150
	ATGTGAACGA AGATCTGGTC GTGACCGAGC TGGAAGTGGC CTATGAAATC	1200
30	TGCCCCGACCT TCCTGGGTGG CCGCGACTGG CCGTCGGCTG CGCTGAACCC	1250
	CGATACTGGC ATCTATTTC A TCCCGCTGAA CAACGCCTGT AGCGGTATGA	1300
35	CGGCTGTCTGA CCAAGAGTTC AGCTCGCTCG ATGTGTATAA CGTCAGCCTC	1350
	GACTATAAAC TGTCGCCCCG TTCGGAAAAC ATGGGCCGTA TCGACGCCAT	1400
	CGACATCAGC ACCGGCCGCA CGCTGTGGTC GGCTGAACGC TACGCCTCGA	1450
40	ACTACGCGCC TGTCCTGTCC ACCGGCGGCG GCGTGCTGTT CAACGGCGGC	1500
	ACCGACCGTT ACTTCCGCGC CCTCAGCCAA GAGACCGGCG AGACGCTGTG	1550
45	GCAGACCCGT CTGGCGACTG TCGCCTCGGG TCAAGCGATT TCCTATGAGA	1600
	TCGACGGCGT GCAATATGTC GCCATCGGGC GCGGCGGCAC CAGCTATGGC	1650
	AGCAACCACA ACCGCGCCCT GACCGAGCGG ATCGACTCGA CCGCCATCGG	1700
50	CAGCGCGATC TATGTCTTTG CTCTGCCGCA GCAGTAA	1737

INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1740 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter oxydans*

STRAIN: DSM 4025

(iv) FEATURE:

FEATURE KEY: CDS

POSITION: 1..1737

SEQUENCING METHOD: E

20 ATGAACCCCA CAACGCTGCT TCGCACCAGC GCGGCCGTGC TATTGCTTAC 50
CGCGCCCGCC GCATTGCGGC AGGTAACCCC GATTACCGAT GAACTGCTGG 100
CGAACCCGCC CGCTGGTGAA TGGATTAACT ACGGCCGCAA CCAAGAAAAC 150
25 TATCGCCACT CGCCCCTGAC CCAGATCACT GCCGACAACG TTGGTCAGTT 200
GCAACTGGTC TGGGCCCCGCG GGATGGAGGC GGGGGCCGTA CAGGTCACGC 250
30 CGATGATCCA TGATGGCGTG ATGTATCTGG CAAACCCCGG TGATGTGATC 300
CAGGCGCTGG ATGCGCAAAC AGGCGATCTG ATCTGGGAAC ACCGCCGCCA 350
ACTGCCCCGCC GTCGCCACGC TAAACGCCCA AGGCGACCGC AAGCGCGGCG 400
35 TCGCCCTTTA CGGCACGAGC CTCTATTTCA GCTCATGGGA CAACCATCTG 450
ATCGCGCTGG ATATGGAGAC GGGCCAGGTC GTATTCGATG TCGAACGTGG 500

	ATCGGGCGAA	GACGGCTTGA	CCAGTAACAC	CACGGGGCCG	ATTGTCGCCA	550
5	ATGGCGTCAT	CGTCGCGGGT	TCCACCTGCC	AATATTCGCC	CTATGGATGC	600
	TTTATCTCGG	GGCACGATTC	CGCGACGGGT	GAGGAGCTGT	GGCGCAACCA	650
	CTTTATCCCG	CAGCCGGGCG	AAGAGGGTGA	CGAGACTTGG	GGCAATGATT	700
10	TCGAGGCGCG	CTGGATGACC	GGCGTCTGGG	GTCAGATCAC	CTATGATCCC	750
	GTGACGAACC	TTGTGTTCTA	TGGCTCGACC	GGCGTGGGCC	CAGCGTCCGA	800
	AACCCAGCGC	GGCACGCCGG	GCGGCACGCT	GTATGGCACC	AACACCCGCT	850
15	TTGCGGTGCG	TCCCGACACG	GGCGAGATTG	TCTGGCGTCA	CCAGACCCTG	900
	CCGCGCGACA	ACTGGGACCA	AGAATGCACG	TTCGAGATGA	TGGTCGCCAA	950
20	CGTCGATGTG	CAACCCTCGG	CCGAGATGGA	GGGTCTGCGC	GCCATCAACC	1000
	CCAATGCGGC	GACGGGCGAG	CGCCGTGTGC	TGACGGGTGC	GCCTTGCAAG	1050
	ACCGGCACGA	TGTGGTCGTT	TGATGCGGCC	TCGGGCGAAT	TCCTGTGGGC	1100
25	GCGTGATACC	AACTACACCA	ATATGATCGC	CTCGATCGAC	GAGACCGGCC	1150
	TTGTGACGGT	GAACGAGGAT	GCGGTGCTGA	AAGAGCTGGA	CGTTGAATAT	1200
30	GACGTCTGCC	CGACCTTCCT	GGGTGGGCGC	GACTGGTCGT	CAGCCGCACT	1250
	GAACCCGGAC	ACCGGCATTT	ACTTCTTGCC	GCTGAACAAT	GCCTGCTACG	1300
	ATATTATGGC	CGTTGATCAA	GAGTTTAGCG	CGCTCGACGT	CTATAACACC	1350
35	AGCGCGACCG	CAAACTCGC	GCCGGGCTTT	GAAAATATGG	GCCGCATCGA	1400
	CGCGATTGAT	ATCAGCACCG	GGCGCACCTT	GTGGTCGGCG	GAGCGCCCTG	1450
40	CGGCGAACTA	CTCGCCCGTT	TTGTCGACGG	CAGGCGGTGT	GGTGTTCAAC	1500
	GGCGGGACCG	ACCGCTATTT	CCGTGCCCTC	AGCCAGGAAA	CCGGCGAGAC	1550
	TTTGTGGCAG	GCCCCGTCTTG	CGACGGTCGC	GACGGGGCAG	GCGATCAGCT	1600
45	ACGAGTTGGA	CGGCGTGCAA	TATATCGCCA	TCGGTGCGGG	CGGTCTGACC	1650
	TATGGCACGC	AATTGAACGC	GCCGCTGGCC	GAGGCAATCG	ATTCGACCTC	1700
50	GGTCGGTAAT	GCGATCTATG	TCTTTGCACT	GCCGCAGTAA		1740

INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 residues

(B) TYPE: amino acid

5 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter oxydans*

STRAIN: DSM 4025

10 (iv) FEATURE:

FEATURE KEY: sig peptide

15 POSITION: -23..-1

SEQUENCING METHOD: E

FEATURE KEY: mat peptide

20 POSITION: 1..556

SEQUENCING METHOD: E

25 Met Lys Pro Thr Ser Leu Leu Trp Ala Ser Ala Gly Ala Leu Ala
-20 -15 -10

30 Leu Leu Ala Ala Pro Ala Phe Ala Gln Val Thr Pro Val Thr Asp
-5 1 5

Glu Leu Leu Ala Asn Pro Pro Ala Gly Glu Trp Ile Ser Tyr Gly
10 15 20

35 Gln Asn Gln Glu Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr
25 30 35

Thr Glu Asn Val Gly Gln Leu Gln Leu Val Trp Ala Arg Gly Met
40 45 50

40 Gln Pro Gly Lys Val Gln Val Thr Pro Leu Ile His Asp Gly Val
55 60 65

	Met	Tyr	Leu	Ala	Asn	Pro	Gly	Asp	Val	Ile	Gln	Ala	Ile	Asp	Ala	
			70					75					80			
5	Lys	Thr	Gly	Asp	Leu	Ile	Trp	Glu	His	Arg	Arg	Gln	Leu	Pro	Asn	
			85					90					95			
	Ile	Ala	Thr	Leu	Asn	Ser	Phe	Gly	Glu	Pro	Thr	Arg	Gly	Met	Ala	
			100					105					110			
10	Leu	Tyr	Gly	Thr	Asn	Val	Tyr	Phe	Val	Ser	Trp	Asp	Asn	His	Leu	
			115					120					125			
	Val	Ala	Leu	Asp	Thr	Ala	Thr	Gly	Gln	Val	Thr	Phe	Asp	Val	Asp	
15			130					135					140			
	Arg	Gly	Gln	Gly	Glu	Asp	Met	Val	Ser	Asn	Ser	Ser	Gly	Pro	Ile	
			145					150					155			
20	Val	Ala	Asn	Gly	Val	Ile	Val	Ala	Gly	Ser	Thr	Cys	Gln	Tyr	Ser	
			160					165					170			
	Pro	Phe	Gly	Cys	Phe	Val	Ser	Gly	His	Asp	Ser	Ala	Thr	Gly	Glu	
			175					180					185			
25	Glu	Leu	Trp	Arg	Asn	Tyr	Phe	Ile	Pro	Arg	Ala	Gly	Glu	Glu	Gly	
			190					195					200			
	Asp	Glu	Thr	Trp	Gly	Asn	Asp	Tyr	Glu	Ala	Arg	Trp	Met	Thr	Gly	
30			205					210					215			
	Ala	Trp	Gly	Gln	Ile	Thr	Tyr	Asp	Pro	Val	Thr	Asn	Leu	Val	His	
			220					225					230			
35	Tyr	Gly	Ser	Thr	Ala	Val	Gly	Pro	Ala	Ser	Glu	Thr	Gln	Arg	Gly	
			235					240					245			
	Thr	Pro	Gly	Gly	Thr	Leu	Tyr	Gly	Thr	Asn	Thr	Arg	Phe	Ala	Val	
			250					255					260			
40	Arg	Pro	Asp	Thr	Gly	Glu	Ile	Val	Trp	Arg	His	Gln	Thr	Leu	Pro	
			265					270					275			
	Arg	Asp	Asn	Trp	Asp	Gln	Glu	Cys	Thr	Phe	Glu	Met	Met	Val	Thr	
45			280					285					290			
	Asn	Val	Asp	Val	Gln	Pro	Ser	Thr	Glu	Met	Glu	Gly	Leu	Gln	Ser	
			295					300					305			
50	Ile	Asn	Pro	Asn	Ala	Ala	Thr	Gly	Glu	Arg	Arg	Val	Leu	Thr	Gly	
			310					315					320			

	Val	Pro	Cys	Lys	Thr	Gly	Thr	Met	Trp	Gln	Phe	Asp	Ala	Glu	Thr
			325					330					335		
5	Gly	Glu	Phe	Leu	Trp	Ala	Arg	Asp	Thr	Asn	Tyr	Gln	Asn	Met	Ile
			340					345					350		
10	Glu	Ser	Ile	Asp	Glu	Asn	Gly	Ile	Val	Thr	Val	Asn	Glu	Asp	Ala
			355					360					365		
	Ile	Leu	Lys	Glu	Leu	Asp	Val	Glu	Tyr	Asp	Val	Cys	Pro	Thr	Phe
			370					375					380		
15	Leu	Gly	Gly	Arg	Asp	Trp	Pro	Ser	Ala	Ala	Leu	Asn	Pro	Asp	Ser
			385					390					395		
	Gly	Ile	Tyr	Phe	Ile	Pro	Leu	Asn	Asn	Val	Cys	Tyr	Asp	Met	Met
			400					405					410		
20	Ala	Val	Asp	Gln	Glu	Phe	Thr	Ser	Met	Asp	Val	Tyr	Asn	Thr	Ser
			415					420					425		
25	Asn	Val	Thr	Lys	Leu	Pro	Pro	Gly	Lys	Asp	Met	Ile	Gly	Arg	Ile
			430					435					440		
	Asp	Ala	Ile	Asp	Ile	Ser	Thr	Gly	Arg	Thr	Leu	Trp	Ser	Val	Glu
			445					450					455		
30	Arg	Ala	Ala	Ala	Asn	Tyr	Ser	Pro	Val	Leu	Ser	Thr	Gly	Gly	Gly
			460					465					470		
	Val	Leu	Phe	Asn	Gly	Gly	Thr	Asp	Arg	Tyr	Phe	Arg	Ala	Leu	Ser
			475					480					485		
35	Gln	Glu	Thr	Gly	Glu	Thr	Leu	Trp	Gln	Thr	Arg	Leu	Ala	Thr	Val
			490					495					500		
40	Ala	Ser	Gly	Gln	Ala	Ile	Ser	Tyr	Glu	Val	Asp	Gly	Met	Gln	Tyr
			505					510					515		
	Val	Ala	Ile	Ala	Gly	Gly	Gly	Val	Ser	Tyr	Gly	Ser	Gly	Leu	Asn
			520					525					530		
45	Ser	Ala	Leu	Ala	Gly	Glu	Arg	Val	Asp	Ser	Thr	Ala	Ile	Gly	Asn
			535					540					545		
	Ala	Val	Tyr	Val	Phe	Ala	Leu	Pro	Gln						
			550					555							
50															

INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 residues

(B) TYPE: amino acid

5 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter oxydans*

STRAIN: DSM 4025

10 (iv) FEATURE:

FEATURE KEY: sig peptide

15 POSITION: -23..-1

SEQUENCING METHOD: S

FEATURE KEY: mat peptide

20 POSITION: 1..556

SEQUENCING METHOD: S

25

Met Lys Thr Ser Ser Leu Leu Val Ala Ser Val Ala Ala Leu Ala
-20 -15 -10

30

Ser Tyr Ser Ser Phe Ala Leu Ala Gln Val Thr Pro Val Thr Asp
-5 1 5

Glu Leu Leu Ala Asn Pro Pro Ala Gly Glu Trp Ile Ser Tyr Gly
10 15 20

35

Gln Asn Gln Glu Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr
25 30 35

Thr Glu Asn Val Gly Gln Leu Gln Leu Val Trp Ala Arg Gly Met
40 45 50

40

Gln Pro Gly Lys Val Gln Val Thr Pro Leu Ile His Asp Gly Val
55 60 65

	Met	Tyr	Leu	Ala	Asn	Pro	Gly	Asp	Val	Ile	Gln	Ala	Ile	Asp	Ala
			70					75					80		
5	Lys	Thr	Gly	Asp	Leu	Ile	Trp	Glu	His	Arg	Arg	Gln	Leu	Pro	Asn
			85					90					95		
	Ile	Ala	Thr	Leu	Asn	Ser	Phe	Gly	Glu	Pro	Thr	Arg	Gly	Met	Ala
			100					105					110		
10	Leu	Tyr	Gly	Thr	Asn	Val	Tyr	Phe	Val	Ser	Trp	Asp	Asn	His	Leu
			115					120					125		
	Val	Ala	Leu	Asp	Thr	Ala	Thr	Gly	Gln	Val	Thr	Phe	Asp	Val	Asp
15			130					135					140		
	Arg	Gly	Gln	Gly	Glu	Asp	Met	Val	Ser	Asn	Ser	Ser	Gly	Pro	Ile
			145					150					155		
20	Val	Ala	Asn	Gly	Val	Ile	Val	Ala	Gly	Ser	Thr	Cys	Gln	Tyr	Ser
			160					165					170		
	Pro	Phe	Gly	Cys	Phe	Val	Ser	Gly	His	Asp	Ser	Ala	Thr	Gly	Glu
			175					180					185		
25	Glu	Leu	Trp	Arg	Asn	Tyr	Phe	Ile	Pro	Arg	Ala	Gly	Glu	Glu	Gly
			190					195					200		
	Asp	Glu	Thr	Trp	Gly	Asn	Asp	Tyr	Glu	Ala	Arg	Trp	Met	Thr	Gly
30			205					210					215		
	Val	Trp	Gly	Gln	Ile	Thr	Tyr	Asp	Pro	Val	Gly	Gly	Leu	Val	His
			220					225					230		
35	Tyr	Gly	Ser	Ser	Ala	Val	Gly	Pro	Ala	Ser	Glu	Thr	Gln	Arg	Gly
			235					240					245		
	Thr	Thr	Gly	Gly	Thr	Met	Tyr	Gly	Thr	Asn	Thr	Arg	Phe	Ala	Val
			250					255					260		
40	Arg	Pro	Glu	Thr	Gly	Glu	Ile	Val	Trp	Arg	His	Gln	Thr	Leu	Pro
			265					270					275		
	Arg	Asp	Asn	Trp	Asp	Gln	Glu	Cys	Thr	Phe	Glu	Met	Met	Val	Ala
45			280					285					290		
	Asn	Val	Asp	Val	Gln	Pro	Ala	Ala	Asp	Met	Asp	Gly	Val	Arg	Ser
			295					300					305		
50	Ile	Asn	Pro	Asn	Ala	Ala	Thr	Gly	Glu	Arg	Arg	Val	Leu	Thr	Gly
			310					315					320		

	Val	Pro	Cys	Lys	Thr	Gly	Thr	Met	Trp	Gln	Phe	Asp	Ala	Glu	Thr
			325					330					335		
5	Gly	Glu	Phe	Leu	Trp	Ala	Arg	Asp	Thr	Ser	Tyr	Glu	Asn	Ile	Ile
			340					345					350		
	Glu	Ser	Ile	Asp	Glu	Asn	Gly	Ile	Val	Thr	Val	Asp	Glu	Ser	Lys
			355					360					365		
10	Val	Leu	Thr	Glu	Leu	Asp	Thr	Pro	Tyr	Asp	Val	Cys	Pro	Leu	Leu
			370					375					380		
	Leu	Gly	Gly	Arg	Asp	Trp	Pro	Ser	Ala	Ala	Leu	Asn	Pro	Asp	Thr
15			385					390					395		
	Gly	Ile	Tyr	Phe	Ile	Pro	Leu	Asn	Asn	Thr	Cys	Met	Asp	Ile	Glu
			400					405					410		
20	Ala	Val	Asp	Gln	Glu	Phe	Ser	Ser	Leu	Asp	Val	Tyr	Asn	Gln	Ser
			415					420					425		
	Leu	Thr	Ala	Lys	Met	Ala	Pro	Gly	Lys	Glu	Leu	Val	Gly	Arg	Ile
			430					435					440		
25	Asp	Ala	Ile	Asp	Ile	Ser	Thr	Gly	Arg	Thr	Leu	Trp	Thr	Ala	Glu
			445					450					455		
	Arg	Glu	Ala	Ser	Asn	Tyr	Ala	Pro	Val	Leu	Ser	Thr	Ala	Gly	Gly
30			460					465					470		
	Val	Leu	Phe	Asn	Gly	Gly	Thr	Asp	Arg	Tyr	Phe	Arg	Ala	Leu	Ser
			475					480					485		
35	Gln	Glu	Thr	Gly	Glu	Thr	Leu	Trp	Gln	Thr	Arg	Leu	Ala	Thr	Val
			490					495					500		
	Ala	Ser	Gly	Gln	Ala	Val	Ser	Tyr	Glu	Ile	Asp	Gly	Val	Gln	Tyr
			505					510					515		
40	Ile	Ala	Ile	Gly	Gly	Gly	Gly	Thr	Thr	Tyr	Gly	Ser	Phe	His	Asn
			520					525					530		
	Arg	Pro	Leu	Ala	Glu	Pro	Val	Asp	Ser	Thr	Ala	Ile	Gly	Asn	Ala
45			535					540					545		
	Met	Tyr	Val	Phe	Ala	Leu	Pro	Gln	Gln						
			550					555							
50															

INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 578 residues

(B) TYPE: amino acid

5 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter oxydans*

STRAIN: DSM 4025

10 (iv) FEATURE:

FEATURE KEY: sig peptide

15 POSITION: -23..-1

SEQUENCING METHOD: S

FEATURE KEY: mat peptide

20 POSITION: 1..555

SEQUENCING METHOD: S

25

Met Lys Leu Thr Thr Leu Leu Gln Ser Ser Ala Ala Leu Leu Val
-20 -15 -10

30 Leu Gly Thr Ile Pro Ala Leu Ala Gln Thr Ala Ile Thr Asp Glu
-5 1 5

Met Leu Ala Asn Pro Pro Ala Gly Glu Trp Ile Asn Tyr Gly Gln
10 15 20

35 Asn Gln Glu Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr Ala
25 30 35

Asp Asn Val Gly Gln Leu Gln Leu Val Trp Ala Arg Gly Met Glu
40 45 50

40

Ala Gly Lys Ile Gln Val Thr Pro Leu Val His Asp Gly Val Met
55 60 65

	Tyr	Leu	Ala	Asn	Pro	Gly	Asp	Val	Ile	Gln	Ala	Ile	Asp	Ala	Ala	
			70					75					80			
5	Thr	Gly	Asp	Leu	Ile	Trp	Glu	His	Arg	Arg	Gln	Leu	Pro	Asn	Ile	
			85					90					95			
	Ala	Thr	Leu	Asn	Ser	Phe	Gly	Glu	Pro	Thr	Arg	Gly	Met	Ala	Leu	
10			100					105					110			
	Tyr	Gly	Thr	Asn	Val	Tyr	Phe	Val	Ser	Trp	Asp	Asn	His	Leu	Val	
			115					120					125			
	Ala	Leu	Asp	Thr	Ser	Thr	Gly	Gln	Val	Val	Phe	Asp	Val	Asp	Arg	
15			130					135					140			
	Gly	Gln	Gly	Thr	Asp	Met	Val	Ser	Asn	Ser	Ser	Gly	Pro	Ile	Val	
			145					150					155			
20	Ala	Asn	Gly	Val	Ile	Val	Ala	Gly	Ser	Thr	Cys	Gln	Tyr	Ser	Pro	
			160					165					170			
	Phe	Gly	Cys	Phe	Val	Ser	Gly	His	Asp	Ser	Ala	Thr	Gly	Glu	Glu	
25			175					180					185			
	Leu	Trp	Arg	Asn	Asn	Phe	Ile	Pro	Arg	Ala	Gly	Glu	Glu	Gly	Asp	
			190					195					200			
	Glu	Thr	Trp	Gly	Asn	Asp	Tyr	Glu	Ala	Arg	Trp	Met	Thr	Gly	Val	
30			205					210					215			
	Trp	Gly	Gln	Ile	Thr	Tyr	Asp	Pro	Val	Gly	Gly	Leu	Val	His	Tyr	
			220					225					230			
35	Gly	Thr	Ser	Ala	Val	Gly	Pro	Ala	Ala	Glu	Ile	Gln	Arg	Gly	Thr	
			235					240					245			
	Val	Gly	Gly	Ser	Met	Tyr	Gly	Thr	Asn	Thr	Arg	Phe	Ala	Val	Arg	
40			250					255					260			
	Pro	Glu	Thr	Gly	Glu	Ile	Val	Trp	Arg	His	Gln	Thr	Leu	Pro	Arg	
			265					270					275			
	Asp	Asn	Trp	Asp	Gln	Glu	Cys	Thr	Phe	Glu	Met	Met	Val	Val	Asn	
45			280					285					290			
	Val	Asp	Val	Gln	Pro	Ser	Ala	Glu	Met	Glu	Gly	Leu	His	Ala	Ile	
			295					300					305			
50	Asn	Pro	Asp	Ala	Ala	Thr	Gly	Glu	Arg	Arg	Val	Val	Thr	Gly	Val	
			310					315					320			

	Pro	Cys	Lys	Asn	Gly	Thr	Met	Trp	Gln	Phe	Asp	Ala	Glu	Thr	Gly
			325					330					335		
5	Glu	Phe	Leu	Trp	Ala	Arg	Asp	Thr	Ser	Tyr	Gln	Asn	Leu	Ile	Glu
			340					345					350		
10	Ser	Val	Asp	Pro	Asp	Gly	Leu	Val	His	Val	Asn	Glu	Asp	Leu	Val
			355					360					365		
	Val	Thr	Glu	Leu	Glu	Val	Ala	Tyr	Glu	Ile	Cys	Pro	Thr	Phe	Leu
			370					375					380		
15	Gly	Gly	Arg	Asp	Trp	Pro	Ser	Ala	Ala	Leu	Asn	Pro	Asp	Thr	Gly
			385					390					395		
	Ile	Tyr	Phe	Ile	Pro	Leu	Asn	Asn	Ala	Cys	Ser	Gly	Met	Thr	Ala
20			400					405					410		
	Val	Asp	Gln	Glu	Phe	Ser	Ser	Leu	Asp	Val	Tyr	Asn	Val	Ser	Leu
			415					420					425		
25	Asp	Tyr	Lys	Leu	Ser	Pro	Gly	Ser	Glu	Asn	Met	Gly	Arg	Ile	Asp
			430					435					440		
	Ala	Ile	Asp	Ile	Ser	Thr	Gly	Arg	Thr	Leu	Trp	Ser	Ala	Glu	Arg
			445					450					455		
30	Tyr	Ala	Ser	Asn	Tyr	Ala	Pro	Val	Leu	Ser	Thr	Gly	Gly	Gly	Val
			460					465					470		
	Leu	Phe	Asn	Gly	Gly	Thr	Asp	Arg	Tyr	Phe	Arg	Ala	Leu	Ser	Gln
35			475					480					485		
	Glu	Thr	Gly	Glu	Thr	Leu	Trp	Gln	Thr	Arg	Leu	Ala	Thr	Val	Ala
			490					495					500		
40	Ser	Gly	Gln	Ala	Ile	Ser	Tyr	Glu	Ile	Asp	Gly	Val	Gln	Tyr	Val
			505					510					515		
	Ala	Ile	Gly	Arg	Gly	Gly	Thr	Ser	Tyr	Gly	Ser	Asn	His	Asn	Arg
			520					525					530		
45	Ala	Leu	Thr	Glu	Arg	Ile	Asp	Ser	Thr	Ala	Ile	Gly	Ser	Ala	Ile
			535					540					545		
50	Tyr	Val	Phe	Ala	Leu	Pro	Gln	Gln							
			550					555							

INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 579 residues

(B) TYPE: amino acid

5 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) ORIGINAL SOURCE:

ORGANISM: *Gluconobacter oxydans*

STRAIN: DSM 4025

10 (iv) FEATURE:

FEATURE KEY: sig peptide

15 POSITION: -23..-1

SEQUENCING METHOD: E

FEATURE KEY: mat peptide

20 POSITION: 1..556

SEQUENCING METHOD: E

25

Met Asn Pro Thr Thr Leu Leu Arg Thr Ser Ala Ala Val Leu Leu
-20 -15 -10

30

Leu Thr Ala Pro Ala Ala Phe Ala Gln Val Thr Pro Ile Thr Asp
-5 1 5

Glu Leu Leu Ala Asn Pro Pro Ala Gly Glu Trp Ile Asn Tyr Gly
10 15 20

35

Arg Asn Gln Glu Asn Tyr Arg His Ser Pro Leu Thr Gln Ile Thr
25 30 35

Ala Asp Asn Val Gly Gln Leu Gln Leu Val Trp Ala Arg Gly Met
40 45 50

40

Glu Ala Gly Ala Val Gln Val Thr Pro Met Ile His Asp Gly Val
55 60 65

	Met	Tyr	Leu	Ala	Asn	Pro	Gly	Asp	Val	Ile	Gln	Ala	Leu	Asp	Ala	
			70					75					80			
5	Gln	Thr	Gly	Asp	Leu	Ile	Trp	Glu	His	Arg	Arg	Gln	Leu	Pro	Ala	
			85					90					95			
	Val	Ala	Thr	Leu	Asn	Ala	Gln	Gly	Asp	Arg	Lys	Arg	Gly	Val	Ala	
			100					105					110			
10	Leu	Tyr	Gly	Thr	Ser	Leu	Tyr	Phe	Ser	Ser	Trp	Asp	Asn	His	Leu	
			115					120					125			
	Ile	Ala	Leu	Asp	Met	Glu	Thr	Gly	Gln	Val	Val	Phe	Asp	Val	Glu	
15			130					135					140			
	Arg	Gly	Ser	Gly	Glu	Asp	Gly	Leu	Thr	Ser	Asn	Thr	Thr	Gly	Pro	
			145					150					155			
20	Ile	Val	Ala	Asn	Gly	Val	Ile	Val	Ala	Gly	Ser	Thr	Cys	Gln	Tyr	
			160					165					170			
	Ser	Pro	Tyr	Gly	Cys	Phe	Ile	Ser	Gly	His	Asp	Ser	Ala	Thr	Gly	
			175					180					185			
25	Glu	Glu	Leu	Trp	Arg	Asn	His	Phe	Ile	Pro	Gln	Pro	Gly	Glu	Glu	
			190					195					200			
	Gly	Asp	Glu	Thr	Trp	Gly	Asn	Asp	Phe	Glu	Ala	Arg	Trp	Met	Thr	
30			205					210					215			
	Gly	Val	Trp	Gly	Gln	Ile	Thr	Tyr	Asp	Pro	Val	Thr	Asn	Leu	Val	
			220					225					230			
35	Phe	Tyr	Gly	Ser	Thr	Gly	Val	Gly	Pro	Ala	Ser	Glu	Thr	Gln	Arg	
			235					240					245			
	Gly	Thr	Pro	Gly	Gly	Thr	Leu	Tyr	Gly	Thr	Asn	Thr	Arg	Phe	Ala	
			250					255					260			
40	Val	Arg	Pro	Asp	Thr	Gly	Glu	Ile	Val	Trp	Arg	His	Gln	Thr	Leu	
			265					270					275			
	Pro	Arg	Asp	Asn	Trp	Asp	Gln	Glu	Cys	Thr	Phe	Glu	Met	Met	Val	
45			280					285					290			
	Ala	Asn	Val	Asp	Val	Gln	Pro	Ser	Ala	Glu	Met	Glu	Gly	Leu	Arg	
			295					300					305			
50	Ala	Ile	Asn	Pro	Asn	Ala	Ala	Thr	Gly	Glu	Arg	Arg	Val	Leu	Thr	
			310					315					320			

	Gly	Ala	Pro	Cys	Lys	Thr	Gly	Thr	Met	Trp	Ser	Phe	Asp	Ala	Ala
			325					330					335		
5	Ser	Gly	Glu	Phe	Leu	Trp	Ala	Arg	Asp	Thr	Asn	Tyr	Thr	Asn	Met
			340					345					350		
10	Ile	Ala	Ser	Ile	Asp	Glu	Thr	Gly	Leu	Val	Thr	Val	Asn	Glu	Asp
			355					360					365		
	Ala	Val	Leu	Lys	Glu	Leu	Asp	Val	Glu	Tyr	Asp	Val	Cys	Pro	Thr
			370					375					380		
15	Phe	Leu	Gly	Gly	Arg	Asp	Trp	Ser	Ser	Ala	Ala	Leu	Asn	Pro	Asp
			385					390					395		
20	Thr	Gly	Ile	Tyr	Phe	Leu	Pro	Leu	Asn	Asn	Ala	Cys	Tyr	Asp	Ile
			400					405					410		
	Met	Ala	Val	Asp	Gln	Glu	Phe	Ser	Ala	Leu	Asp	Val	Tyr	Asn	Thr
			415					420					425		
25	Ser	Ala	Thr	Ala	Lys	Leu	Ala	Pro	Gly	Phe	Glu	Asn	Met	Gly	Arg
			430					435					440		
	Ile	Asp	Ala	Ile	Asp	Ile	Ser	Thr	Gly	Arg	Thr	Leu	Trp	Ser	Ala
			445					450					455		
30	Glu	Arg	Pro	Ala	Ala	Asn	Tyr	Ser	Pro	Val	Leu	Ser	Thr	Ala	Gly
			460					465					470		
35	Gly	Val	Val	Phe	Asn	Gly	Gly	Thr	Asp	Arg	Tyr	Phe	Arg	Ala	Leu
			475					480					485		
	Ser	Gln	Glu	Thr	Gly	Glu	Thr	Leu	Trp	Gln	Ala	Arg	Leu	Ala	Thr
			490					495					500		
40	Val	Ala	Thr	Gly	Gln	Ala	Ile	Ser	Tyr	Glu	Leu	Asp	Gly	Val	Gln
			505					510					515		
	Tyr	Ile	Ala	Ile	Gly	Ala	Gly	Gly	Leu	Thr	Tyr	Gly	Thr	Gln	Leu
			520					525					530		
45	Asn	Ala	Pro	Leu	Ala	Glu	Ala	Ile	Asp	Ser	Thr	Ser	Val	Gly	Asn
			535					540					545		
50	Ala	Ile	Tyr	Val	Phe	Ala	Leu	Pro	Gln						
			550					555							

INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 bases

(B) TYPE: nucleotide

5 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ORIGINAL SOURCE: synthetic oligonucleotide

CATGAAAATA AAAACAGGTG CACGCATCCT CGCATTATCC GCATTAACGA 50
10 CGATGATGTT TTCCGCCTCG GCTCTGCCCC AG 82

INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 83 bases

(B) TYPE: nucleotide

(C) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(iii) ORIGINAL SOURCE: synthetic oligonucleotide

20

GTTACCTGGG CGAGAGCCGA GCGGAAAAC ATCATCGTCG TTAATGCGGA 50
TAATGCGAGG ATGCGTGCAC CTGTTTTTAT TTT 83

INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 residues

(B) TYPE: amino acid

5 (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) ORIGINAL SOURCE: *E. coli*

(iv) FEATURE:

FEATURE KEY: sig peptide

10 POSITION: 1..26

FEATURE METHOD: S

15 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu
1 5 10 15
Thr Thr Met Met Phe Ser Ala Ser Ala Leu Ala Gln
20 25 27

20 INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 bases

(B) TYPE: nucleotide

(C) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(iii) ORIGINAL SOURCE: synthetic oligonucleotide

30 GTTAGCGCGG TGGATCCCCA TTGGAGG 27